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Database :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  equence:
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                                                                                                                                                                                                                                                                                                                                                          and is derived
                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                         No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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5::
5::
7::
8::
9::
110:
113::
113::
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                               Published_Applications_AA: *
                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
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Copyright (c) 1993 - 2003 Compuo
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                                                                                                                                                           1884
1907
160
442
    4545
44
119
607
607
637
                                                                                       468
468
393
609
793
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27.566 Million cell updates/sec
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 US-10-090-185-10

US-09-815-242-10740

10 US-09-825-302-780

10 US-09-873-403-2

10 US-09-864-761-36590

10 US-09-865-242-13379

10 US-09-815-242-13682

10 US-09-815-242-12058
                                                                                                                           US-09-824-053-3

US-09-998-284-2

US-09-824-053-10

US-09-824-053-10

US-09-785-770A-17

US-09-785-770A-16

US-09-786-770A-16

US-09-764-864-1020

US-09-731-872-283

US-09-731-872-283

US-09-331-872-283

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sequence 2, Appli
Sequence 10, Appl
Sequence 10740, A
Sequence 780, Appl
Sequence 36, Appli
Sequence 3650, A
Sequence 246, App
Sequence 13879, A
Sequence 13882, A
Sequence 13882, A
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Sequence
Sequence
Sequence
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                                                                                                                                         3, Appli
2, Appli
31, Appl
10, Appl
17, Appl
16, Appl
16, Appl
1020, Ap
286, App
283, App
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42.9	42.9	42.9	42.9	42.9	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.8	45.5	45.5	45.5	45.5	45.5	45.5	46.1	46.1	46.8	46.8	46.8
104	104	64	64	15	26926	2310	2273	618	618	451	260	217	156	419	504	503	461	420	250	91	520	516	4636	669	388
9	9	10	10	12	9	10	10	10	10	Q	9	9	10	10	9	9	9	9	9	10	9	9	10	10	9
US-09-796-692-2057	US-09-796-692-1793	US-09-764-877-1246	US-09-864-761-43603	US-10-085-027-4	US-09-759-508B-2	US-09-995-542-10	US-09-995-542-12	US-09-970-516-4	US-09-817-676A-14	US-09-738-626-3550	US-09-764-868-1030	US-09-738-626-5827	US-09-864-761-39604	US-09-741-669-415	US-10-007-814-4	US-10-007-814-2	US-09-738-626-5041	US-10-007-814-6	US-10-007-814-8	US-09-864-761-36754	US-10-067-534-4	US-10-067-534-3	US-09-835-996A-33	US-09-801-196-28	US-09-975-139-9
2057,	793, A		Sequence 43603, A	Sequence 4, Appli	2, Ap	10,	12,	4,	Sequence 14, Appl	Sequence 3550, Ap	•	Sequence 5827, Ap	39604	Sequence 415, App	Sequence 4, Appli	Sequence 2, Appli	504	6	Sequence 8, Appli	e 36	4	, Ap	ω ,	e 28	Sequence 9, Appli

ALIGNMENTS

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RESULT 1
US-09-824-053-3
; Sequence 3, Application US/09824053
; Patent No. US20020106725A1
; GENERAL INFORMATION:
                                                                  REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (202) 955-1926
TELEPHAX: (202) 778-2201
TELEPAX: (202) 778-2201
TELEX: NO. US20020106725A1e
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               COMPUTER: IBM PC COMPACTIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,053
FILING DATE: 03-Apr-2001
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/669,304
FILING DATE: <Unknown>
PRIOR APPLICATION NUMBER: 08/669,304
FILING DATE: <Unknown>
APPLICATION NUMBER: 28,562
REGISTRATION NUMBER: 28,562
REGISTRATION NUMBER: 28,562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20006-1109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Peter Stougaard
Ole Cai Hansen
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1900 K STREET: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 20006-1109
STRANDEDNESS:
                         TYPE: amino
                                              LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Hunton & Williams
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unknown
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TOPOLOGY: unknown

HOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-824-053-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT; ORGANISM: Chondrus crispus US-09-998-284-2
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US-09-998-284-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     URRENT APPLICATION NUMBER: US/09/998,284
CURRENT FILING DATE: 2001-11-30
PRIOR PREPARATION NUMBER: PCT/IB00/00829
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: GB 9913050.2
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/09824053
Patent No. US20020106725A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: POULSEN, et al.
TITLE OF INVENTION: COMPOSITION
YILE REFERENCE: 674509-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 DLPMSPRGVIASNLHF 234
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                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,053
EILING DATE: 03-Apr-2001
CLASSIFICATION: -Unknown>
                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Hunton & Williams
STREET: 1900 K Street, N.W.
                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Peter Stougaard
                                                                                                                                                                                                    CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1109
APPLICATION NUMBER: 08/669,304
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Pred. No. 2.
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2.5e-05;
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; SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-09-824-053-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09824053 Patent No. US20020106725A1 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                          REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 955-1926
TELEPAX: (202) 778-2201
TELEX: No. US2002016725Ale
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 778-2201
TELEX: NO. US20020106725A1e
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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219 DLPMSPRGVIASNLHF 234
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/669,304
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Stanislaus Aksman
REGISTRATION NUMBER: 28,562
REGISTRATION NUMBER: 78,562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20006-1109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Hunton & Williams
STREET: 1900 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 955-1926
                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Peter Stougaard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1109
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/824,053 FILING DATE: 03-Apr-2001 CLASSIFICATION: <Unknown>
                                                                                 TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Stanislaus Aksman
REGISTRATION NUMBER: 28,562
REFERENCE/DOCKET NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
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                                                               TOPOLOGY: unknown
                                                                                                                          LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ole Cai Hansen
                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.48;
93.88;
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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2.5e-05;
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Sequence 16, Application US/09785770A stent No. US20020103360A1
ENERAL INFORMATION:
APPLICANT: Barnes, Thomas M.
APPLICANT: Barnes, Thomas M.
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                                                                                                                       US-09-785-770A-16
                                                                                                                                                                                                                  APPLICANT: Barnes, Thomas M.
TITLE OF INVENTION: A NOVEL PROTEIN RELATE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 07334-328001
COURTENT APPLICATION NUMBER: US/09/785,770A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/387,462
PRIOR APPLICATION NUMBER: US 09/145,056
PRIOR FILING DATE: 1999-09-01
PRIOR FILING DATE: 1998-09-01
NUMBER OF SEQ ID NOS: 24
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Patent No. US20020103360A1

RNERAL INFORMATION:
APPLICANT: Pan, Yang
APPLICANT: Pan, Yang
APPLICANT: Barnes, Thomas M.
APPLICANT: Barnes, Thomas M.
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 07334-328001
CURRENT APPLICATION NUMBER: US/09/785,770A
CURRENT APPLICATION NUMBER: US/09/785,770A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 09/387,462
PRIOR APPLICATION NUMBER: US 09/387,462
PRIOR FILING DATE: 1999-09-01
PRIOR FILING DATE: 1998-09-01
PRIOR FILING DATE: 1998-09-01
                                                    Matches
                                                                                                                                                        SOFTWARE: PatentIn Ver. 4.0
SEQ ID NO 16
LENGTH: 1907
TYPE: PRT
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                                                                                     Query Match
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Best Local Similarity
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                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1804 DLPLHPRGFLPGHAPF 1819
                                                  Local Similarity es 7; Conserv
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              1 DLPMSPRGVIASNLXF 16
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43.8%;
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93.88;
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Pred. No.
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Pred. No.
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Pred. No. 7.4e-07;
                                                  Mismatches
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No. 92;
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RESULT 9
US-09-731-872-283
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US-09-764-864-1020
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SEQ ID NO 286
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Patent No. US20020102604A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1020
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                                                                                                                                                                     Matches 6; Conserv
                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/731,872
CURRENT FILING DATE: 2000-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
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CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                                                                                       NAME/KEY: UNSURE
LOCATION: 132
OTHER INFORMATION: Xaa - Pro, Arg
                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: SIGNAL
LOCATION: -21..-1
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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37.5%;
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Pred. No. 27;
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Pred. No. 8
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US-10-090-185-10
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CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 09/292,097
PRIOR FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PERL Program
SEQ ID NO 2
                                      GENERAL INFORMATION:
                                                      Sequence 10, Application US/10090185 Publication No. US20020197647A1
                                                                                                                                                                                                                                             Matches
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Best Local (
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SOFTWARE: Patent.pm
SEQ ID NO 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REF
CURRENT APPLICATION NUMBER: US/09/731,872
CURRENT FILING DATE: 2000-12-07
FRIOR APPLICATION NUMBER: US 60/169,629
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 1999-13-08
PRIOR FILING DATE: 1999-13-08
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APPLICANT: Kaser, Matthew R.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: TAPASIN-LIKE PROTEIN
FILE REFERENCE: PC-0002-1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: SIGNAL
LOCATION: -21..-1
9-731-872-283
APPLICANT: Zhang, Xiaokui
APPLICANT: Wrzeszczynska, Melissa
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DTHER INFORMATION: 103348CD1
09-933-561-2
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TYPE: PRT
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ORGANISM: Homo sapiens
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les 6; Conserv
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Pred. No.
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29;
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; LOCATION: (1)...(609); OTHER INFORMATION: Xaa US-09-815-242-10740
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                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: ELITA.0114
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT ETLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-05-23
PRIOR FILLING DATE: 2000-05-23
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/243,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILLING DATE: 2000-11-27
PRIOR PILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILLING DATE: 2001-02-16
PRIOR FILLING DATE: 2001-02-16
PRIOR FILLING DATE: 2001-02-16
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; Patent No. US20020061569A1
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PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 10
LENGTH: 393
                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10740
LENGTH: 609
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                    Query Match
Best Local :
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Best Local
Matches
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APPLICANT: Darnell Jr., James E
APPLICANT: DARNEL DARNEL DARNEL DARNEL DARNEL DARNEL DARNEL DE DE LINVENTION: METHODS FOR, IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVATO
TITLE OF INVENTION: INVERACTIONS
FILE REFERENCE: 600-1-253
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                        ORGANISM: Enterococcus faecalis FEATURE:
                                                                                                                                                 NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 DLPMSPR 352
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Similarity 7; Conserv
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Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu, H. Howard
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  Conservative
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100.0%; Pred. No.
                    49.4%;
43.8%;
                                                                                                         Any Amino Acid
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  ű,
Score 38; DB
Pred. No. 57;
3; Mismatches
                      DB 10;
57;
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                                          Length 609;
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  Indels
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432 DIPAAPRGVPQIEVSF 447

DLPMSPRGVIASNLXF 16

RESULT 13 US-09-925-302-780

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US-09-925-302-780
                                     RESULT 15
US-09-864-761-36590
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LENGTH: 793
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Sequence 36590, Application US/09864761 Patent No. US20020048763A1
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA104
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/873,403
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/625,139
PRIOR FILING DATE: 2000-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Srivstava, Pramod K
TITLE OF INVENTION: COMPLEXES OF ALPHA (2) MACROGLOBULIN AND ANTIGENIC
TITLE OF INVENTION: MOLECULES FOR IMMUNOTHERAPY
FILE REFERENCE: 8449-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/925,302
URRENT FILING DATE: 2001-08-10
RIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
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                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0
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2460 DIPQQPMGIIA 2470
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Local Similarity 54.5%;
les 6; Conservative
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100.0%; Pred. No.
tive 0; Mismatc
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Pred. No. 5
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5.2e+02;
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OTHER INFORMATION: EXPRESSED IN HBL100,
OTHER INFORMATION: EXPRESSED IN LUNG, S
OTHER INFORMATION: EXPRESSED IN LUNG, S
OTHER INFORMATION: EXPRESSED IN BRAIN,
OTHER INFORMATION: EXPRESSED IN BTAIN,
OTHER INFORMATION: EXPRESSED IN BTAIN,
OTHER INFORMATION: EXPRESSED IN BOUE MA
OTHER INFORMATION: EXPRESSED IN HELA, S
OTHER INFORMATION: EXPRESSED IN MOLT INFORMATION: EXPRESSED IN HELA, S
OTHER INFORMATION: EXPRESSED INFORM
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        Matches
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CURRENT FILING DATE: 2001-05-23
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PRIOR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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Hanzel, David K.
        Conservative
                                                                                                                                                                                                                    NN: EXPRESSED IN HBL100, SIGNAL = 1.3

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

NN: EXPRESSED IN LUNG, SIGNAL = 1.2

NN: EXPRESSED IN BRAIN, SIGNAL = 1.2

NN: EXPRESSED IN PLACENTA, SIGNAL = 1.3

NN: EXPRESSED IN BT474, SIGNAL = 1.3

NN: EXPRESSED IN BONE MARROW, SIGNAL = 1.3

NN: EXPRESSED IN HELA, SIGNAL = 1.3

NN: EXPRESSED IN HELA, SIGNAL = 1.3

NN: EXPRESSED IN HELAR, SIGNAL = 1.2

NN: EXPRESSED IN HEART, SIGNAL = 1.2
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                                        HIT: P77672, EVAI
HIT: BE960561.1,
Score 37; DB 10; Length 4.4; Pred. No. 4.6; 2; Mismatches 3; Indels
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RESULT 17
US-09-815-242-13379
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US-09-867-550-246
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                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                          PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                  RPPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells and TITLE OF INVENTION: Thereby FILE REFERENCE: 21402-01.3 (Cura-313) CURRENT APPLICATION NUMBER: US209/867,550 CURRENT FILING DATE: 2001-09-20 PRIOR APPLICATION NUMBER: USSN 60/208,427 PRIOR APPLICATION NUMBER: USSN 60/208,427 PRIOR FILING DATE: 2000-05-30 NUMBER OF SEQ ID NOS: 2125 OPTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: wherein Xaa may be any one of Arg or Gln or Leu or OTHER INFORMATION: Thr or Lys or Ala or Val or Glu or Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: VARIANT LOCATION: (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 119
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 MAPRGIVAASV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 MSPRGVIASNL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity es 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
                                      APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PMVPRGLAVSSL 15
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Trawick, John D.
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Conley, Pamela
                                                                                                                                                                                                                                                                                                                             Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                 Carr, Grant J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                        2000-10-23
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Pred. No. 14;
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RESULT 19
US-09-815-242-12058
; Sequence 12058, Application US/09815242
; Patent NO. US20020061569A1
. GENERAL INFORMATION:
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Best Local Similarity
Watches 6; Conserve
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13379
LENGTH: 607
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                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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APPLICANT:
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PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                       LENGTH: 607
TYPE: PRT
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                                                                                                                                                    431 DIPAAPRGIPQIEVTF 446
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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Trawick, John D.
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Zyskind, Judith W.
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                                                                                                                                                                                                                                     Score 37; DB Pred. No. 84;
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Pred. No.
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84;
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION INVEST: 60/191,078

FILE REFERENCE: ELITRA, 011A

CURRENT APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

RIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-2

PRIOR APPLICATION NUMBER: 60/259,308

PRIOR FILING DATE: 2001-02-16

SOFTWARE: FESTESEQ TO NOS: 14110

SOFTWARE: FESTESEQ TO Windows Version 4.0

SOFTWARE: FESTESEQ FOR Windows Version 4.0

CRGANISM: Pseudomonas meruginosa

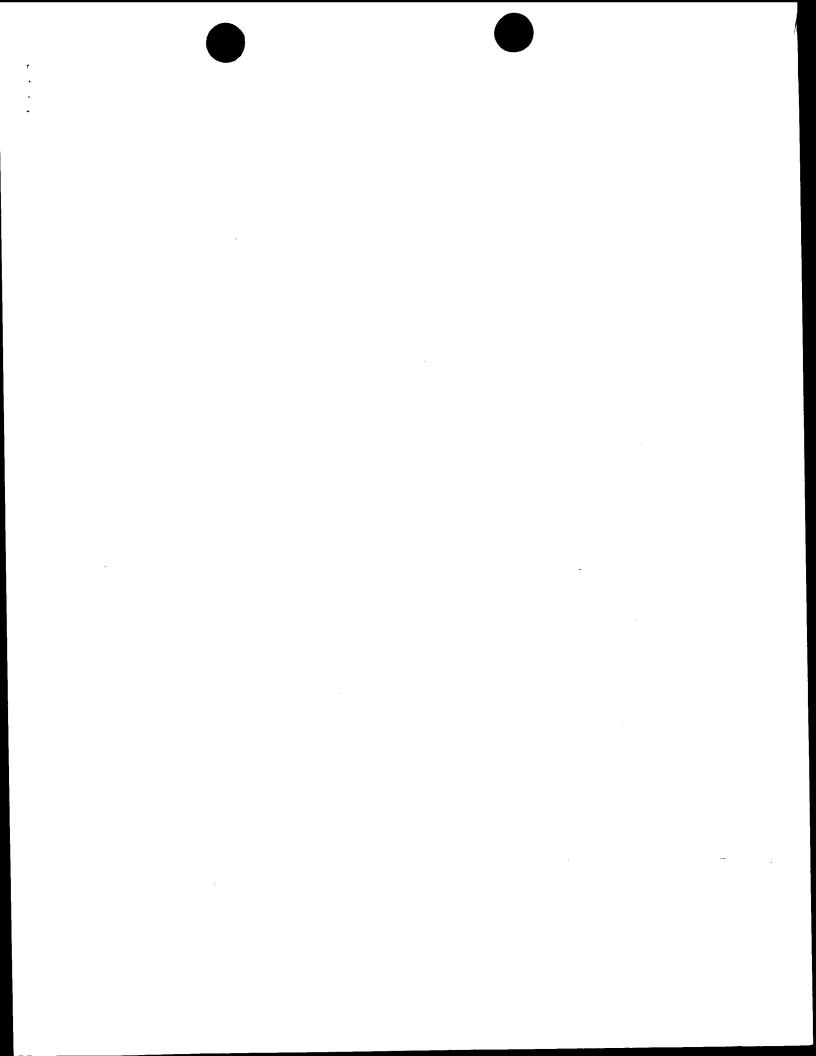
US-09-815-242-12058
                                                                                                                                                                             requence 9. Application US/09975139
atent No. US20020155460A1
GENERAL INFORMATION:
APPLICANT: Genencor International, Inc.
APPLICANT: Schellenberger, Volker
APPLICANT: Mari Jonald
APPLICANT: Morrison, Thomas B.
TITLE OF INVENTION: INFORMATION RICH LIBRARIES
FILE REFERENCE: 23633-7060
CURRENT APPLICATION NUMBER: US/09/975,139
CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/239,476
PRIOR APPLICATION UNMBER: US 60/239,476
PRIOR FILING DATE: 2000-10-10
SOFTMARE: FASTSEQ ID NOS: 10
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 388
TYPE: PRT
ORGANISM: Yersinia enterolitica
                                                                                                                      ; FEATURE:
; OTHER INFORMATION: AmpC protein
US-09-975-139-9
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           Query Match 46.9
Best Local Similarity 54.9
Matches 6; Conservative
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Yamamoto, Robert T.
Xu, H. Howard
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                                 46.8%; Score 36; DB 9; Length 388; 54.5%; Pred. No. 76;
             4.
             Mismatches
        1; Indels
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     0;
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Gaps
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Qy 3 PMSPRGVIASN 13

Db 304 PINPQGVIADS 314

Search completed: January 2, 2003, 12:10:23

Job time: 12 secs
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GenCore version 5.1.3 Compugen Ltd

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Title:
Perfect score:
Sequence:
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Maximum DB
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No.
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Maximum Match 100%
Listing first 45 summaries
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seq
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1. /SIDS2/gcgdata/gc
2. /SIDS2/gcgdata/gc
3. /SIDS2/gcgdata/gc
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length: 2000000000
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Match
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT;*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT;*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT;*
                                                                                                                                                                                                                                 Length
      187
230
230
2506
2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
                                                                                                         546
546
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                                                                                                                                                                                                                                 BB
                                                                                                                                                                                                                                 IJ
                         AAY83619
AAU02192
AAB59205
ABP30454
AAY91319
ABP28247
ABG07191
                                                                                                                                                                    AAW20070
AAW20076
      ABG30064
                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Search time 35 Seconds
(without alignments)
60.915 Million cell updates/sec
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Streptococcus poly Group B Streptococ Streptococcus poly Novel human diagno
                                                                                                HOX3, a hexose oxi
Hexose oxidase, an
Synthetic hexose o
Synthetic hexose o
Chondrus cripus he
                                                                                                                                                                                                                               Description
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Chicken leucocytoz	AAR97866	17	1132	50.6	39	45
101510	AAE15174	23	770	50.6	ω 9	44
	AAR 19964	S	770	•	39	
_	AAR82993	16	770	•	39	42
tapasin.	ABB08402	23	468	•	39	
protein s	AAB92557	22	468	•	39	40
secreted	AAG89163	22	468	•	39	39
_	AAG89166	22	442	•	39	8
_	AAM40079	22	338	50.6	39	37
	AAB41889	21	319	•	39	36
	AAY30811	20	308	•	39	G
polyp	ABB90285	23	307	•	39	34
Human gene 1 encod	AAE09683	22	277	•	39	W W
secret	AAU20491	22	268	•	39	32
Human novel secre	AAU16067	22	160	•	39	ω L
റ.	AAG35596	21	155	٠	39	30
Human immune/haema	AAM84414	22	152	•	39	29
	ABG26574	22	151	50.6	39	28
reproductiv	AAM96691		149	•	39	27
Human testicular a	ABB96590	22	149	•	39	26
Sequence encoded b	AAP70470	8	148	•	39	25
Ö	AAP70471	œ	144	•	39	24
secret	ABB12095	22	143	•	39	23
human	AAU23057	22	113	50.6	39	22
novel f	AAU20801	22	103	•	39	21
	AAM89886	22	97	•	39	20
-	AAM94707	22	84	٠	39	19
	AAU22735	22	84	•	39	18
	ABG24042	22	70	•	39	17
Novel human secre	AAU32407		1194	•	40	16
	ABG61824	23	1193	51.9	40	
Human protein sequ	AAM25602		1193	٠	40	
Tomato DMT protein	AAU72763	23	255	•	40	
_	ABP41781		245	•	40	12
Novel human diagno	ABG23334	22	185	51.9	40	

ALIGNMENTS

RESULT 1 AAW20070

AAW20070 standard; peptide; 16

Š

Hansen OC, Chondrus crispus. Hexose oxidase; Chondrus crispus; marine algae; recombinant; antimicrobial; antioxidant; food preparation; dairy product; starc beverage; animal feed; silage; sugar reduction; cosmetics; dental; 07-JUN-1995; 04-JUN-1996; 19-DEC-1996 WO9640935-A1 Misc-difference HOX3, a hexose oxidase derived antimicrobial/antioxidant peptide. AAW20070; (BIOT-) BIOTEKNOLOGISK INST toothpaste; dough; lactone production. 12-SEP-1997 (first entry) Stougaard P; 9508-0476910 96WO-DK00238 Location/Qualifiers /note= "x= any naturally occurring amino acid" starch;

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RESULT 2
AAW20076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW20068-75 are small peptides derived from hexose oxidase (HO) of the marine algae species Chondrus crispus. Hexose oxidase and peptides having HO activity are useful in the production of food products, e.g. dairy products, starch-containing food products (dough) and non-dairy beverages. HO and active peptide fragments have antimicrobial and antioxidant properties and act by removing all the oxygen in a food packaging. HO and peptides of HO can also be used in an animal feed, especially silage. Further uses are to reduce, or analyse, the sugar content in a food, in the production of cosmetics, tooth care products or a pharmaceutical product and in lactone production. HO can be a quality and purity level which renders polypeptide suitable for
AAW20076 shows the hexose oxidase (HO) enzyme of the marine algae species Chondrus crispus. HO is useful in the production of food products, e.g. dairy products, starch-containing food products (dough) and non-dairy beverages. HO and active peptide fragments have
                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                04-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                  19-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant production of polypeptide having hexose oxidase activity - used in food preparations as antibacterial and antioxidant agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-052332/05
                                                                                                                    Recombinant production of polypeptide having hexose oxidase activity - used in food preparations as antibacterial and antioxidant agent
                                                                                                                                                                                          WPI; 1997-052332/05
                                                                                                                                                                                                                             Hansen OC,
                                                                                                                                                                                                                                                                                               07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                    WO9640935-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Chondrus crispus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antimicrobial; antioxidant; food preparation; dairy product; starch;
beverage; animal feed; silage; sugar reduction; cosmetics; dental;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW20076 standard; Protein;
                                                                                                                                                                                                                                                           (BIOT-) BIOTEKNOLOGISK INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     toothpaste; dough;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hexose oxidase; Chondrus crispus; marine algae; recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hexose oxidase, an antimicrobial/antioxidant agent.
                                                                                      Example 3.5; Page 95-97; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DLPMSPRGVIASNLXF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLPMSPRGVIASNLXF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                         AAT76552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 99; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    purposes.
                                                                                                                                                                                                                         Stougaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                               95US-0476910
                                                                                                                                                                                                                                                                                                                                96WO-DK00238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lactone production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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9.9e-07;
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AAY83619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                        Wild type hexose oxidase can be produced by isolating a nucleotide sequence coding for hexose oxidase naturally produced by an organism and modifying the sequence so that the modified sequence is expressed, under identical conditions, at a level at least 10% higher than the non-modified sequence. The method is useful for producing hexose oxidase in prokaryotic and eukaryotic cells. Previous methods of producing hexose oxidase were to isolate the enzyme from a source that naturally produces the enzyme, using host organisms which produce a relatively low level of expression. Therefore, industrial produced method which produces at least 250 mg enzyme per liter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antimicrobial and antioxidant properties and act by removing all the oxygen in a food packaging. HO and peptides of HO can also be used in an animal feed, especially silage. Further uses are to reduce, or analyse, the sugar content in a food, in the production of cosmetics, tooth care products or a pharmaceutical product and in lactone production. HO can be recombinantly produced in industrially appropriate quantities, and at a quality and purity level which renders the polypeptide suitable for industrial purposes.
                                                                                                                                                                                                                                   Disclosure; Page 28-29; 42pp; English.
                                                                                                                                                                                                                                                                             Nucleic acid fragment useful for producing large amounts of hexose oxidase comprises nucleotide sequence encoding hexose oxidase that
                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1008651-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY83619 standard; Protein;
                              of fermentation medium.
                                                                                                                                                                                                                                                                modified by at least one codon
                                                                                                                                                                                                                                                                                                                                                                         Stougaard P,
                                                                                                                                                                                                                                                                                                                                                                                                        (BIOT-) BIOTEKNOLOGISK INST
                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prokaryote;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hexose oxidase; production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic hexose oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 DLPMSPRGVIASNLHF 234
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                                                                                                                                                                                                                                                                                                                                              2000-389309/34.
                                                                                                                                                                                                                                                                                                                             AAZ94011.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546 AA;
 546 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eukaryote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                           Pedersen
                                                                                                                                                                                                                                                                                                                                                                                                                                       98DK-0001630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99EP-0204068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.4%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                           LH,
                                                                                                                                                                                                                                                                                                                                                                           Wolff AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fermentation; synthetic; modification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      546 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 75; L
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Poulsen U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .3e-05;
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                                                                                                                                                                                                                                                                                                                                                                            Hansen OC;
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                                                                                                                                                                                                                                                                                that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Query Match
Best Local Similarity

97.4%; 93.8%;

Score Pred.

75; No.

DB 21; 5.3e-05;

Length 546;

Sequence

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8888888888888888888888888888888888
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AAU02192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g x a
                                CC a soluble or membrane associated intracellular protein of interest (POI)

Cf from a cell involving contacting a cell comprising a soluble or membrane

Cc associated intracellular POI with a membrane extracting composition (I)

CC and causing the POI to be released from the cell in a soluble form. The

CC method is useful for releasing POI, such as an interleukin I receptor

CC antagonist (IL-Ira) which involves contacting a transformed cell

CC comprising IL-Ira with (I) and causing IL-Ira to be released from the

CC transformed cell, in a soluble form. The method is also useful for

CC screening mutated cells or transformed cells producing elevated levels of

CC intracellular POI. The method is used to release a POI for manufacturing

CC food products, such as beverages, preparation of detergents, and in

CC baking as a dough improving agent. The method obtains a fast, specific

CC and economically efficient extraction of a soluble or membrane associated

CC intracellular POI without the use of conventional cell disruption

CC techniques. The resulting cell extract contains less contaminating

CC intracellular POI can be recovered from a eukaryotic host organism such

CC as yeast, before glycosylation takes place. The method can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents the amino acid sequence of synthetic hexose oxidase (D-hexose:02-oxireductase, EC 1.1.3.5), also referred to as HOX. The native HOX gene was altered using site-directed mutagenesis in order to match the codon usage to known codon preferences of biotechnologically relevant yeasts, such as Pichia sp., to facilitate high level production of HOX in these organisms. The invention involves a method for releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ...., seaweed; nexose oxidase; interleukin I receptor antagonist; food manufacturing; beverage; detergent; baking; dough improving D-hexose:O2-oxireductase; EC 1.1.3.5.
as yeast, before glycosylation takes place. The method can be used prevent contact of intracellular POI with the extracellular growth medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Fig 6; 108pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Releasing soluble or membrane associated intracellular protein from a cell for manufacturing food, comprises contacting the cell with a membrane extracting composition and causing the protein to be released
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chondrus crispus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic hexose oxidase (HOX) amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-367695/38
N-PSDB; AASO6173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-NOV-2000; 2000WO-IB01886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in soluble form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zargahi MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DANI-) DANISCO AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kjaerulff S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99GB-0027801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Madrid SM,
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ABP30454;

02-JUL-2002

(first entry)

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RESULT 5
AAB59205
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           ABP30454
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                        RESULT 6
                                                                                                        Matches
                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                          The present invention relates to a new anti-fouling composition. The composition involves a surface coating material, a hexose oxidase enzyme obtained from a marine organism and a substrate for the enzyme. The anti-fouling composition is useful as a coating formulated for treating a surface, e.g. outdoor wood work, external surface of a central heating system, or a hull of a marine vessel. It is also useful as an anti-fouling agent for marine structures exposed to seawater flora and fauna.
                                                                                                                                                                                                                                                                                                         New anti-fouling composition, useful as a coating for treating different surfaces, e.g. outdoor woodwork, external surface of central heating system, or a hull of a marine vessel
                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chondrus cripus hexose oxidase enzyme protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
 ABP30454 standard;
                                                                                                                                                                                                                                                                                  Claim 5; Page 35-36; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-112148/12.
                                                                                                                                                                                                                                                                                                                                                                                 Poulsen CH,
                                                                                                                                                                                                                                                                                                                                                                                                        (DANI-) DANISCO AS
                                                                                                                                                                                                                                                                                                                                                                                                                                04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUN-2000; 2000WO-IB00829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200075293-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chondrus cripus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hexose oxidase; marine alga; anti-fouling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB59205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB59205
                                                            219
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                                                                                                                    Local
                                                                               1 DLPMSPRGVIASNLXF 16
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                                                        l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                       546 AA;
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                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              99GB-0013050
Protein; 187 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein; 546 AA
                                                                                                                   97.4%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.4%;
                                                                                                        0
                                                                                                                 Score 75; I
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 75; DB 22;
Pred. No. 5.3e-05;
                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                             DB 22;
                                                                                                                   3e-05;
                                                                                                                           Length 546;
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RESULT 7
AAY91319
ID AAY9
XX
AC AAY9
AC AAY9
AC AAY9
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                                                                                                                                                                                                                                                                                                                                                                      CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (C (Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (C (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the proteins have antibacterial and antiinflammatory comprising one of 5483 sequences (S1), given in the protein of the sequences of medicamentory comprising one of 5483 sequences (S1), given in the manufacture of medicaments for comprising (I) are used in the manufacture of medicaments for comprising (I) are used to detect streptococcus in a composition comprising (I) are used to detect streptococcus in a composition comprising (I) or a nucleic acid encoding (I), may be used to detect may be mening (I) may be used to streptococcus that is prevented or treated may be meningitis. Nucleic composition composition. The disease caused by composition or diagnostic composition. The disease caused by composition or diagnostic composition. The disease caused by composition or diagnostic composition or the disease caused by composition or diagnostic composition. The disease caused by composition or diagnostic composition or the disease caused by composition or diagnostic composition. The disease caused by composition or diagnostic composition or diagnostic composition. The disease caused by composition or diagnostic composition or diagnostic composition. The disease caused by composition or diagnostic composition or diagnostic composition. The disease caused by composition or diagnostic composition or diagnostic composition. The disease caused by composition or diagnostic composition o
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Tettelin H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                 Group B
                                                 30-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 4137; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABN71085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-352536/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200234771-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus polypeptide SEQ ID NO 10084.
                                                                                                                AAY91319 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-OCT-2001; 2001WO-GB04789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                             Streptococcus proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR-) CHIRON SPA.
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                                                                                                                                                                                                                               G
                                                                                                                                                                                                                               SPRGVIASNLXF 16
                                                                                                                                                                                                SPRGVIANKLVF
                                                                                                                                                                                                                                                              Similarity
9; Conserv
                  Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                187 AA;
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                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                             57.1%;
75.0%;
               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Margarit Ros YI,
                                                                                                                230
                                                                                                                                                                                                                                                                               Score 44; DB:
Pred. No. 6.1;
                 sequence
                                                                                                                                                                                                                                                               Mismatches
                  SEQ
                                                                                                                                                                                                                                                                                              DB 23;
                  ID NO:47.
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                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                            Length 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser
                                                                                                                                                                                                                                                              0;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                              antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUL-1998;
19-MAR-1999;
                                                                29-OCT-2001;
                                                                                                                                                                                                                                                                                                02-JUL-2002
                                                                                                                                                                                                                                                                                                                                ABP28247;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               56 SPRGVIANKLVF 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPRGVIASNLXF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-195299/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
9; Conserv
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27-OCT-2000;
24-NOV-2000;
07-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Group B Streptococcus; Streptococcus agalactiae; protein antigen; vaccine; screening; immunogen; detection; diagnosis; infection; antibody; affibody; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus polypeptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 1; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Group B Streptococcus protein, useful as vaccine, for diagnosis of 
Streptococcal infections and for screening of antibodies or affibodies
                                                                                                                                                                                                                                                                                                          Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP28247 standard; Protein; 230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MICR-) MICROBIAL TECHNICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
2000GB-0026333.
2000GB-0028727.
2001GB-0005640.
                                                                                                                          2001WO-GB04789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98GB-0016335.
99US-0125163.
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                                                                                                                                                                                                                                                                                                                                                                        infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanniffy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB Pred. No. 7.7; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5670
                                                                                                                                                                                                                                                                                                                                                                    meningitis; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
7.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG07191 standard; Protein; 2506 AA.
              Drmanac RT,
                                                                                   31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                         WO200175067-A2
                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #7182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 3729; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                      30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                             food supplement;
                                                                                                                                                                                                                                                                                                                                                                    13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABN68878.
                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-352536/38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENO-) INST GENOMIC RES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 SPRGVIASNLXF 16
                                                                                                                                                                                                                                                                           chromosome mapping; gene mapping; gene therapy;
upplement; medical imaging; diagnostic; genetic (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
9; Conserv
              Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                   2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.18;
75.08;
            Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 23; Pred. No. 7.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC polypertide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical company of sites expressing (II). (I) and (II) are useful for treating cC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC specification, but was obtained in electronic format directly from WIPO CC at first wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
N-PSDB; AAS94251
                WPI; 2001-639362/73
                                                  Drmanac RT, Liu C,
                                                                                                                     31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                         30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                               11-OCT-2001.
                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #30055.
                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG30064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG30064 standard; Protein; 2506 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 37550; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73.
N-PSDB; AAS71378.
                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         745 LPAPPRGVVQRRLTF 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 LPMSPRGVIASNLXF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.5%;
                                                  Tang YT

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 22;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutations
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  EXEX E
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CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC (II). (II) is useful for generating antibodies against it, detecting or
CC (Quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC The polypeptide and polynucleotide sequences have applications in
CC disorders involving aberrant protein expression or biological activity.

The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits to assess biodiversity
and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                            31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 60423; 103pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
New isolated polynucleotide and encoded polypeptides, useful
                                      WPI; 2001-639362/73.
N-PSDB; AAS87521.
                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                              11-OCT-2001
                                                                                                                                                                                                                                                                                                                     WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #23325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG23334 standard; Protein; 185 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymerase chain reaction (PCR) primers, oligomers, and and gene mapping, and in recombinant production of (II).
                                                                                                Drmanac RT,
                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            745 LPAPPRGVVQRRLTF 759
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8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2506 AA;
                                                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                2000US-0649167
                                                                                                                                                                                                2000US-0540217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 22;
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .6e+02;
es 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2506;
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  in
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PIN PARKET
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ABP41781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for identifying expressed genes. (1) is useful in gene therapy techniques (11) crestore normal activity of (II) or to treat disease states involving (11). (II) is useful for generating antibodies against it, detecting or compared to the sequence of the sequence or compared to the sequence of sites expressing (II) and its binding partners are useful in medical compared to the sequence of sites expressing (II). (I) and (II) are useful for treating the sequences of the polypeptide and polynucleotide sequences have applications in compared to the sequence of the sequences of data and products dependent on DNA and to produce other types of data and products dependent on DNA and compared to the sequences. ABG00010-ABG30377 represent novel human cold sequences data for this patent did not appear in the printed consecution, but was obtained in electronic format directly from WIPO constitutions that the sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                              gene therapy; chromosome mapping;
antibody preparation; cytostatic;
antiinflammatory; gynaecological;
                                                                                                                                                                                                                                                                                                                    Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ovarian antigen HLDAS11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 53693; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                   (HUMA-) HUMAN GENOME SCI INC
                                                                         07-JUN-2000;
                                                                                                               07-JUN-2001; 2001WO-US18569.
                                                                                                                                                                                           W0200200677-A1
                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP41781 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PMSPRGVIAS 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                         2000US-209467P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:2913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                  reproductive
                                                                                                                                                                                                                                                                                    forensic analysis;
immunomodulatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                                                                                                      neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Birse CE,

Rosen CA;

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CCCXXXTTTTXXX
                                                                                                   shock syndrome), inflammatory conditions (e.g., mastitus, ophoritis and covaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), communodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), communodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), communodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), communodeficiencies, cardiovascular disorders, cardiovascular disorders, cardiovascular disorders, cardiovascular disorders, cardiovascular disorders, cardiovascular disorders and urinary system disorders. Ovarian antigen polypeptides and cardiovaluals and susceptivity. The polynucleotides may community of the polynucleotides may community of the polynucleotides may cardiovaluals and in forensic analysis, and the completification of individuals and in forensic analysis, and the completification of the diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention.

CC Note: The sequence data for this patent did not form part of the printed content of the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine disorders, inferting, chiamydia, HIV, toxoplasmosis, and toxic above syndromes (e.g., chiamydia, HIV, toxoplasmosis, and toxic above syndromes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; SEQ ID No 2913; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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Query Match Best Local S Matches 7 Sequence ftp.wipo.int/pub/published_pct_sequences. 245 AA; 51.9%;

Pred. No. 44; Mismatches

Length 245 Indels

6,

0,

0;

0

Similarity 7; Conserv

Conservative

RESULT 13

AAU72763 standard; Protein; 255 AA

AAU72763;

26-FEB-2002 (first entry)

Demeter; DMT; Atropos; ATR; 5-methylcytosine glycosylase; Tomato DMT protein related sequence #2.

DNA demethylation; flowering time; endosperm development; MEDEA transgenic plant; transcription modulation;

Lycopersicon esculentum.

01-NOV-2001

23-APR-2001; 2001WO-US13059

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated polynucleotide sequence or their complement encoding a polypeptide having a sequence at least 40% complement encoding a polypeptide having a sequence at least 40% compared to DMT (DEMETER, previously known as ATROPOS (ATR)) Domain A, B compared to the control of a promoter at least 70% identical to compared the comprising the polynucleotide or comprising a heterologous compared to the control of a promoter at least 70% identical to DMT 5' flanking sequence, DMT 3' flanking sequence or an 5' untranslated compared to the conding a DMT-like protein and a transgenic plant comprising a composition of DMT, a host cell comprising an exogenous polynucleotide encoding a DMT-like protein. The method comprises introducing the cassette into a host cell preferably Agrobacterium by sexual cross, and selecting a host cell with modulated transcription, where the protein is capable of exhibiting at least one of the following composition in a plant results in adelay in flowering time, introduction of the protein in an arabidopsis leaf results in evapression of the protein in an Arabidopsis leaf results in expression of the MEDEA gene. The polynucleotide is useful for detecting a nucleic acid in a sample. Compared the composition of the protein in a related to 5-methylcytosine glycosylases and regulates compared transcription of the present a num-like protein in a present a num-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                neuroprotective; antidepressant; nootropic; antiparkinsonian; infection immunostimulant; gene therapy; antisense therapy; vaccine; inflammation antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoletic disorder; platelet disorder; asthma;
                                                                                                                     Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fingicide; antimutagen; cardiovascular; antianemic; anaemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; antiaggregant; antialiergic; antialsethmatic; antiabetic; cytostatic; dermatological; antialiergic; antialsethmatic; antidabetic; cytostatic;
  thrombocytopaenia; osteoporosis; severe combined
                                                                                                                                                                                                                                                                                               Human protein sequence SEQ ID NO:1117.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM25602 standard; Protein; 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence represents a DMT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 96; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide that control plant development comprising a sequence having a specific homology to DEMETER domains A,B or {\tt C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-2000; 2000US-0553690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 DLPSSPSSVVSSEI 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DLPMSPRGVIASNL 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hannon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okamuro JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Length 255;
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immunodeficiency;
                                                                                  inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>.</u>
                                                                                                          infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Q
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-DEC-1999;
21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopietic disorders, inflammation, genetic diseases, haematopietic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-457603/49.
N-PSDB; AAH99543.
                                                                                                                                                                                                                                                                                                                                                                                                                                    anaemia, platelet disorders thrombocytopaenia, wounds, burns, u osteoporosis, severe combined immunodeficiency, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depress. Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200153455-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                               1113 DLPLHPRGFLPGHAPF 1128
                                                                                                                                                                                                                                                                                                                   ches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells they are expressed in, such as: antiinflammatory; antirheumatic antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 230; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurological disorder.
              Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
                                                 Prostate cancer-associated protein #25.
                                                                                     15-AUG-2002 (first entry)
                                                                                                                                                       ABG61824 standard; Protein; 1193 AA.
                                                                                                                                                                                                                                                                                                                                                ry Match
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-DEC-2000; 2000WO-US35017.
                                                                                                                                                                                                                                                                                                             Local Similarity es 7; Conserv
                                                                                                                                                                                                                                                                              1 DLPMSPRGVIASNLXF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                      1193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0471275.
2000US-0488725.
2000US-0552317.
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                 51.9%;
43.8%;
                                                                                                                                                                                                                                                                                                               Score 40; DB 22; Pred. No. 2.6e+02; Wismatches 6;
                                                                                                                                                                                                                                                                                                                                                  Length 1193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             burns, ulcers,
                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                   0;
   밁
                                                                                                                                                                                                                                                                                                                                                                                        AAU32407
                                                                                                                                                                                              RESULT 16
                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer as well as for identifying modulators of prostate cancer as well as for identifying modulators of prostate cancer or agents that inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gish KC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200230268-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia
Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopolesis; nerve tissue regeneration;
                                                   Novel human secreted protein #2898.
                                                                                                                          AAU32407;
                                                                                                                                                             AAU32407 standard; Protein; 1194 AA
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       prostate cancer. The nucleic acid sequences are particularly useful
in gene therapy, as a vaccine or in antisense applications.
ABG61800-ABG61944 represent prostate cancer-associated proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to methods of detecting a prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; Page 321; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are expressed in a prostate tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JAN-2001;
16-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-2001; 2001WO-US32045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-2002.
                                                                                         18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EOSB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-2001;
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                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                1 DLPMSPRGVIASNLXF 16
                                                                                                                                                                                                                                                 DLPLHPRGFLPGHAPF 1128
                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK92139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mack DH, Wilson KE,
                                                                                                                                                                                                                                                                                                                                                                                          1193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-281922P.
2001US-286214P.
2001US-0847046.
2001US-288589P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001US-263957P.
2001US-276791P.
2001US-276888P.
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0733288.
2000US-0733742.
                                                                                                                                                                                                                                                                                                                                     51.9%;
                                                                                                                                                                                                                                                                                                                 Score 40; Db zz,
Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Afar D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hevezi P;
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                                                                                                                                                                                                                                                                                                                    Indels
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Gaps

0,

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RESULT 17
ABG24042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or the nucleic acids encoding the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically censineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and centerapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in concerned expression and/or nerve tissue growth or regeneration; inflammatory agents; and in treatment of leukaemias. ANJU39510-ANJU33304 represent the amino acid concerned the amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                     atches
                                                                                                                                                                                                                                                                                                                                                                   1114 DLPLHPRGFLPGHAPF 1129
30-MAR-2001; 2001WO-US08631
                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                   ABG24042 standard; Protein; 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 605-606; 765pp; English.
                                  11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-611725/70.
                                                                                                  Homo sapiens
                                                                                                                                                                                Novel human diagnostic protein #24033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences of novel human secreted proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-APR-2001; 2001WO-US08656.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200179449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                  1 DLPMSPRGVIASNLXF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 22; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1194;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                             RESULT 18
AAU22735
                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
            17-JAN-2001; 2001WO-US01328
                                                                                                                                                                                                                                                                              AAU22735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polymerase chain reaction (PCR) primers oligomers, and for chromosome CC polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical consisting of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed constitution, but was obtained in electronic format directly from WIPO at the content of the format content of the format content of the content of 
                                                                                                                                                                                                                                                                                  Human; prostate cancer antigen; cytostatic; uropathic; diagnostic; reproductive system; chromosomal marker; forensic; urinary disorde chronic nephritis; blood-related disorder; thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-2001
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02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate cancer antigen, Seq ID No 254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                    WO200155316-A2
                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU22735 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22; Length 70;
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4-AUG-2
18-AUG-2
22-AUC
22-AUC
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
14-SEP-2000
14-SEP-2000
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21-SEP-2000
21-SEP-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
27-SEP-2000
27-SEP-2000
29-SEP-2000
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30-AUG-2000;
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11-NO
      Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the reproductive system including prostate cancer
                                                WPI; 2001-451929/48.
N-PSDB; AAS40102.
                                                                                              Rosen
                                                                                                                         ( HUMA - )
                                                                                            CA,
                                                                                                                          HUMAN GENOME SCI
                                                                                            Barash SC,
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RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel isolated human prostate cancer antigen polynucleotides (I) and polypeptides (II). (I) and (II) are useful for preventing, treating or amelitorating a medical condition when administered. (I), (II) and the antibody to (II) are useful for treating, preventing and/or prognosing disorders related to the reproductive system including prostate cancers, urinary disorders e.g. chronic nephritis; and blood-related disorders e.g. thrombosis. (II) can be used for testing and detection e.g. as a chromosomal marker and in forensics. (I) and the anti-(II) antibody can be used in testing and detection in immunoassays. AAU22702-AAU22913 represent the human prostate cancer antigen amino acid sequences, and related amino acid sequences for the part of the printed specification, but was obtained in electronic format different process.
                                                                                                                                                                                                                                                                                  17-JAN-2001; 2001WO-US01339
                                                                                                                                                                                                                                                                                                           02-AUG-2001
                                                                                                                                                                                                                                                                                                                                  WO200155320-A2
                                                                                                                                                                                                                                                                                                                                                                              cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                               Human reproductive system related antigen SEQ ID NO: 3365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM94707 standard; Protein; 84 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                          Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID No 254; 546pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 IPLSPAGVIA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for testing and detection e.g. diagnosis
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70.0%;
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Pred. No. 20;
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                                                                                                                The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
 AAM89886 standard; Protein; 97 AA.
                                                                                                                                                                                           WPI; 2001-465570/50.
N-PSDB; AAL00677.
                                                                                                  Sequence
                                                                                                                                                      Claim 11; SEQ ID NO 3365; 1297pp + Sequence Listing; English.
                                                                                                                                                                    Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000;
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Human immune/haematopoietic antigen SEQ ID NO:17479.
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                                      (first entry)
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.

WO200157182-A2

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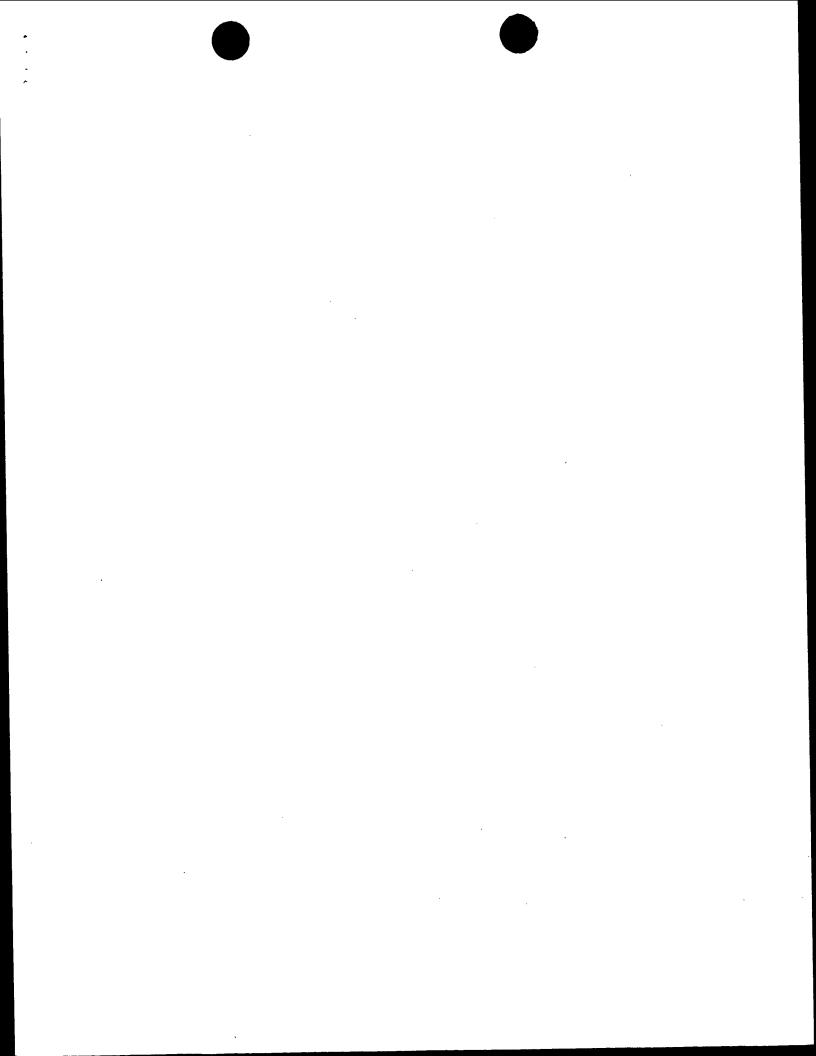
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Result

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48.1	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	49.4	50.6	50.6	50.6	50.6	0				97.4	Match
307	4544	4544	770	770	770	770	770	770	770	770	770	770	770	770	770	770	393	771	771	770	770	770	468	16	546	16	Length
4	N	_	Ç	4	۵	4	4	4	ω	ω	ω	ω	N	N	_	Ļ	4	۳	<u>,</u>	4	Ц	щ	4	4	4	4	BG
US-08-858-207A-481	-08	-486-5	PCT-US95-17025-12	US-09-526-542-2	US-08-956-653A-12	US-09-556-273-8	US-09-364-970-5	US-09-364-970-3	US-08-948-547-12	US-09-012-710-8	US-08-956-869-12	\vdash	US-08-820-754-12	US-08-852-091-12	US-08-416-581B-9	US-08-369-796-12	US-09-387-418A-10	US-08-781-890-14	US-08-276-099A-14	US-09-087-465-6	US-08-416-581B-5	US-08-416-581B-1	US-09-292-097-2	US-08-669-304-10		US-08-669-304-3	ID
Sequence 481, App	52,		12	2,	12,	ω,	ر د	3, 2	12,	, B	12,	12,	12,	12	O	12	10,	14,	14,	6	G	1,	2, 7	10,	<u>3</u> 1	Sequence 3, Appli	Description

45	44	43	42	41	40	39	38	37	36	35	4	·w	32	31	30	29	28
34	34	34	34	35	35	35	36	36	36	36	36	37	37	37	37	37	37
44.2	44.2	44.2	44.2	45.5	45.5	45.5	46.8	46.8	46.8	46.8	46.8	48.1	48.1	48.1	48.1	48.1	48.1
244	244	241	31	317	317	298	669	669	669	564	366	2588	2584	861	861	616	607
N	Ľ	ω	ω	σ	ب	N	4	4	w	4	4	w	w	,_	ب	4	ພ
US-08-878-283-3	US-08-289-699A-3	US-08-834-776A-2	US-08-926-842B-58	PCT-US93-08528-27	US-08-118-270-27	US-09-006-535-3	US-09-391-104-29	US-09-521-220-3	US-08-704-711A-3	US-09-211-704A-8	US-09-134-001C-4799	US-08-936-135-2	US-08-936-135-4	US-08-484-106-18	US-08-484-105-18	US-09-134-001C-3646	US-08-472-534-5
ω	ω.	N	58	27	27	ω	29	Sequence 3, Appli	ω	Sequence 8, Appli		N	A	18,	•	364	Sequence 5, Appli

ALIGNMENTS

RESULT 1 US-08-669-304-3

Sequence 3, Application US/08669304 Patent No. 6251626

GENERAL INFORMATION:
APPLICANT: Peter Stougaard
APPLICANT: Ole Cai Hansen
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A
TITLE OF INVENTION: METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME

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US-08-669-304-3
                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Hunton & Williams
STREET: 1900 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006-1109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,304
FILING DATE: 12 July 1996
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,910
FILING DATE: 7 June 1995
ATTONNEY/ACENT INFORMATION:
NAME: Stanislaus Aksman
REGISTRATION NUMBER: 28,562
REFERENCE /DOCKET NUMBER: 28,562
REFERENCE /DOCKET NUMBER: 28,562
Query Match 97.4%; Score 75; DB 4; I
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 320.000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 955-1926
TELEFAX: (202) 778-2201
TELEX: No. 6521626e
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: unk
TOPOLOGY: unknown
                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                            16 amino acids
                                                                                                                                                         unknown
                                                                                                                                                                           unknown
                                              Length 16;
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Indels

0

Gaps

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RESULT 2
US-08-669-304-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-669-304-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: NO. 6251626

INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                           Sequence 10, Application US/08669304 Patent No. 6251626
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/476,910
FILING DATE: 7 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: Stanislaus Aksman
REGISTRATION NUMBER: 28,562
REFERENCE/DOCKET NUMBER: 320.000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 955-1926
                                                                                                                                                                                                                                                                                                                                                                             tches
                                   APPLICANT: Peter Stougaard
APPLICANT: Ole Cai Hansen
TITLE ON TUVENTION: RECOMBINANT HEXOSE OXIDASE, A
TITLE OF INVENTION: METHOD OF PRODUCING SAME AND USE OF SUCH ENZYME
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 12 July 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Peter Stougaard
APPLICANT: Ole Cai Hansen
TITLE OF INVENTION: RECOMBI
TITLE OF INVENTION: METHOD
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   219 DLPMSPRGVIASNLHF 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 20006-1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202) 955-193
TELEFAX: (202) 778-2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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nes 15; Conserv
  STREET:
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                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                          1 DLPMSPRGVIASNLXF 16
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1900 K Street, N.W.
1900 K Street, N.W.
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                    Hunton & Williams
                                                                                                                                                                                                                                                                                                                                                                                                97.4%;
93.8%;
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Pred. No. 1.8e-05;
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; TOPOLOGY: unknown ; MOLECULE TYPE: peptide US-08-669-304-10
                                                                                                                              ; OTHER INFORMATION: 103348CD1 US-09-292-097-2
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09292097B Patent No. 6322977
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Best Local S
                                                                  Matches
                                                                                                                                                                                                                                 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                 APPLICANT: Lal, Preeti
APPLICANT: Kaser, Matthew, R.
APPLICANT: Baughn, Mariah, R.
TITLE OF INVENTION: TAPASIN-LIKE PROTEIN
FILE REFERENCE: PC-0002 US
                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/292,097B
CURRENT FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 955-1
TELEFAX: (202) 778-220
TELEX: NO. 6251626e
INFORMATION FOR SEQ ID NO:
                                                                                                                                                               LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 955-1926
TELEPHONE: (202) 778-2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 7 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: Stanislaus Aksman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,910
FILING DATE: 7 June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
176 NLPLSPQGTVRTAVEF 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08, FILING DATE: 12 July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
COUNTRY: U.S.A.
                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DLPMSPRGVIASNLWF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                               1 DLPMSPRGVIASNLXF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DLPMSPRGVIASNLXF 16
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                                                                6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                 50.6%;
37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.1%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/669,304
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                                                                   6
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Pred. No. 4.
                                                                                 Score 39; DB Pred. No. 39;
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                                                                   Mismatches
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4.6e-07;
1;
                                                                                                   DB 4;
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                                                                                                   Length 468;
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RESULT 5

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US-08-416-581B-5
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                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08416581B Patent No. 5719042
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Applic Patent No. 5719042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                   APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Akira, Shizuo
TITLE OF INVENTION: TRANSCRIPTION FACTOR APRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TRANSCRIPTION FACTOR APRE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Akira, Shizuo
                                                                            ZIP: 20037
OMPUMBER -
                                                                                                                                                                                                                                                                                                                                                                                                                                  723 DLPMSPRAL 731
                                                                                                                                            CITY: Washington
                                                                                                                                                                STREET:
                                                                                                                               STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 6-65825/1994 FILING DATE: 04-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 04-AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DLPMSPRGV 9
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                                                                                                                                                                E: SUGHRUE, MION, ZINN, MACPEAK & SEAS 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           770 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-1995
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77.8%;
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Query Match
Best Local Similarity
Thes 7; Conserva
                                                                                                                                                  RESULT 8
US-08-276-099A-14
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                                                                                                 Sequence 14, Application US/08276099A Patent No. 5591825 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 770
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09087465A Patent No. 6160092 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Darnell Jr., James E
APPLICANT: KUTIYAN, John
TITLE OF INVENTION: A CRYSTAL OF THE CORE PORTION OF A STAT AND METHODS OF
TITLE OF INVENTION: USE
FILE REFERENCE: 600-1-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/087,465A CURRENT FILING DATE: 1998-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Vinkemeier, Uwe APPLICANT: Chen, Xiaomin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
            APPLICANT: McKnight, Steven L
APPLICANT: Hou, Jinzhao
TITLE OF INVENTION: INTERLEUKIN-4:
TITLE OF INVENTION: BINDING ASSAYS
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 6-65825/1994
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
 CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION:
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tes 7; Conserv
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REGISTRATION NUMBER: 3:
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                                                                                                                                                                                                                                                                                           Conservative
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(202)293-7860
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ADDRESS
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                                                                                                                                                                                                                                                                                                          50.6%;
77.8%;
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                                             INTERLEUKIN-4 SIGNAL TRANSDUCERS AND
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                                                                                                                                                                                                                                                                                        Score 39; DB
Pred. No. 70;
1; Mismatches
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Pred. No. 70;
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US-08-781-890-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
TELEFAX: 910 277299
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,099A
FILING DATE: 15-JUL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59451-1/RAO
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: McKnight, Steven L
APPLICANT: Hou, JInzhao
TITLE OF INVENTION: INTERLEUKIN-4:
TITLE OF INVENTION: BINDING ASSAYS
                  FILING DATE: 15-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard Aro
                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,099
FILING DATE: 15-JUL-1994
                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                             STREET: 4 Emwarum.
CITY: San Francisco
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CITY: San Francisco
STATE: California
                                                                                                                   APPLICATION NUMBER: FILING DATE: 05-JAN CLASSIFICATION: 530
                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Local Similarity 77.8%;
les 7; Conservative
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    REGISTRATION NUMBER:
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Richard Aron
NUMBER: 36,627
                                                                                                                                        05-JAN-1997
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RESULT 11
US-08-369-796-12
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; LENGTH: 393
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-387-418A-10
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                                                                                                                                                                                                                            Sequence 12, Application US/08369796 Patent No. 5716622
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF TRANSCRIPTIONAL ACTIVAT FITLE OF INVENTION: INTERACTIONS
FILE REFERENCE: 600-1-253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zhang, Xiaoku
APPLICANT: Wrzeszczynska
APPLICANT: Horvath, Curt
APPLICANT: Darnell Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/387,418A CURRENT FILING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: A-59451-1/RAO TELECOMMUNICATION INFORMATION:
                                                                                                                                       APPLICANT: James E. Darnell
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Zhong Zhong
                                                                  CORRESPONDENCE ADDRESS
                                                                                  TITLE OF INVENTIÓN: FÚNCTIONALLY ACTIVE REGIONS OF SIGNAL TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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CITY: Hackensack
STATE: New Jersey
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                                  STREET:
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                                                   ADDRESSEE:
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Horvath, Curt M
                                  411 Hackensack Avenue
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                                                                                                                                                                                           James E. Darnell, Jr
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                                                   Klauber & Jackson
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77.8%;
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48;
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COUNTRY:

USA

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RESULT 12
US-08-416-581B-9
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  TELEFAX: (202)293-7060

TELEFAX: (202)293-7060

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Kishimoto, Tadamitsu
APPLICANT: Akira, Shizuo
TITLE OF INVENTION: TRANSCRIPTION FACTOR APRE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/08416581B Patent No. 5719042
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
                                                                                               NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                 APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-65825/1994
FILING DATE: 04-APR-1994
ATTORNEY/ACENT INFORMATION:
NAME: 14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 410
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 133521
NFORMATION FOR SEQ ID NO:
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LENGTH: 770 amino acid
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APPLICATION NUMBER: US
FILING DATE: 06-JAN-19
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20037
amino acid

    SUGHRUE, MION, ZINN, MACPEAK & SEAS
    2100 Pennsylvania Avenue, N.W.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.4%; Score 38; DB 1; Length 770; 100.0%; Pred. No. 1e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/369,796
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; Sequence 12, Application US/08820754
; Patent No. 5976835
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                                                RESULT 14
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US-08-852-091-12
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                                                                                                                                                              Matches
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08852091 Patent No. 5883228
                                                                                                                                                                                                                                                                                                                      TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
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                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/30
FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
                                                                                                723 DLPMSPR 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                             Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINEET: 411 Hackensack Avenue CITY: Hackensack STATE: New Y-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0
FILING DATE: 06-MAY-1997
CLASSIFICATION: 424
                                                                                                                            1 DLPMSPR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                              LENGTH:
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GY: linear
                                                                                                                                                                                                                                                                                           770 amino acids
                                                                                                                                                             Conservative
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Curt M. Horvath
Zhong Zhong
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                                                                                                                                                                            100.0%;
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                                                                                                                                                                     49.4%; Score 38; DB 2; Length 770; 100.0%; Pred. No. 1e+02;
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                                                                                                                                                           Mismatches
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                                                               Sequence 12, Application Patent No. 6013475
GENERAL INFORMATION:
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TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 11-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION NUMBER: US 08/126,588
APPLICATION NUMBER: US 08/126,588
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FILING DATE: 19-MAR-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
-820-754-12
APPLICANT:
              APPLICANT:
                            APPLICANT:
                                                  APPLICANT:
                                                                                                                                                                                          723 DLPMSPR 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 411 Hacker
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO US93/02569 FILING DATE: 19-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                            1 DLPMSPR 7
                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                    Application US/08956652
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Wen, Zilong
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                                                                                                                                                                                                                                                               Conservative
           Darnell Jr., James E. Schindler, Christian W. Fu, Xian-Yuan
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                                                                                                                                                                                                                                                                                                                                                   protein
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                                                                                                                                                                                                                                                              49.4%; Score 38; DB 2; Length 770; 100.0%; Pred. No. 1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 07/854,296
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; MOLECULE TYPE: protein US-08-956-652-12
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                                                                                                                                                                                  Sequence 12, Appli-
Patent No. 6030808
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APPLICATION NUMBER: US 08/
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 19-MAR-1992
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                      GENERAL INFORMATION:
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TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIL
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US
FILING DATE: 19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                      APPLICANT: Darnell Jr., James E.
APPLICANT: Schindler, Christian W.
APPLICANT: Fu, Xian-Yuan
APPLICANT: Wen, Zilong
APPLICANT: Zhong, Zhong
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TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
              TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN UNMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/956,652
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                                                                                                                                                                                                                                                                                                                                                                                49.4%; Score 38; DB 3; Length 770; 100.0%; Pred. No. 1e+02; tive 0; Mismatches 0; Indels
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ADDRESSEE:

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US-09-012-710-8
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
FRIGHH: 770 amino acids
                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09012710 Patent No. 6087478
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                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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APPLICATION NUMBER: WO US9
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David
                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                    APPLICANT: Moarefi, Ismail
APPLICANT: Darnell, Jr., James E.
APPLICANT: Kurlyan, John
TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A
TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
RUMBER OF SEQUENCES: 13
                                                                                                                               ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                     723 DLPMSPR 729
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APPLICATION NUMBER: US 0:
FILING DATE: 19-MAR-1992
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                                             COUNTRY: UZIP: 07601
                                                                            CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/212,185
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                                                                                                         411 Hackensack Avenue, 4th Floor
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                                                              USA
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411 Hackensack Avenue
                                                                                                                                                                                                                                                                                Vinkemeier, Uwe
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US-08-948-547-12
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amin
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                                                                   APPLICATION NUMBER: US/08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
                 APPLICATION NUMBER: US 07/854,296 FILING DATE: 19-MAR-1992 PRIOR APPLICATION DATA:
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APPLICANT:
                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/948,547
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
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STREET: 41.
STREET: Hackensack
CITY: Hackensack
CTATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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 APPLICATION NUMBER:
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
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CLASSIFICATION:
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Wen, Zilong
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WO US93/02569
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CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 770
TYPE: PAT
ORGANISM: Mus musculus
US-09-364-970-3
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US-09-364-970-5
GENERAL INFORMATION:

APPLICANT: Bromberg, Jacqueline
TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTION FACTORS AND THEIR
TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING
TITLE OF INVENTION: DYSEROLIFERATIVE CELLULAR CHANGES
FILE REFERENCE: 600-1-252
FILE REFERENCE: 600-1-252
CURRENT APPLICATION NUMBER: US/09/364,970
CURRENT FILING DATE: 1999-07-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09364970 Patent No. 6235873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                      Sequence 5, Application US/09364970 Patent No. 6235873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 49.4%; Score 38; DB 4; Length 770; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bromberg, Jacqueline TITLE OF INVENTION: CONSTITUTIVELY ACTIVE TRANSCRIPTIÓN FACTORS AND THEIR TITLE OF INVENTION: USES FOR IDENTIFYING MODULATORS OF ACTIVITY INCLUDING TITLE OF INVENTION: DYSPROLIFERATIVE CELLULAR CHANGES FILE REFERENCE: 600-1-252
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TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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TypOLOGY: line

(OLECTION)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
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REFERENCE/DOCKET NUMBER: 600-1-073 CIP
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nes 7; Conserv
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; LENGTH: 770
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-364-970-5

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
Oy 1 DLPMSPR 7

Oy 1 DLPMSPR 7

Db 723 DLPMSPR 729

Search completed: January 2, 2003, 12:05:31
Job time: 36 secs
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GenCore version 5.1.3 Coppright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

January 2, 2003, 12:03:04 ; Search time 16 Seconds (without alignments) 96.134 Million cell upda

cell updates/sec

Title: US-09-824-053-3 77

Sequence: Perfect score: 1 DLPMSPRGVIASNLXF 16

ing table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	9 5	4	ω	2	1	Result
				37													38	38	39	39	39	40	40	41	41	42	43	43	Score
48.1		48.1	48.1	48.1	48.1	49.4		49.4	49.4	49.4	49.4	49.4		49.4	49.4	49.4	9.	9	50.6	0		۲.	۲.	ω.	ω.	٠.	5	ū	Query Match
500	485	368	362	245	196	4545	4544	4543	1305	770	684	670	479	363	334	334	328	272	770	206	113	407	295	416	416	416	184	184	Length
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C84791	F71275	G75425	T41785	AB1807	T50018	S25111	S02392	A53102	T31096	149508	G90473	A75542	S72582	G72854	G72024	E86597	E95421	C64009	A54444	A64339	151025	G84309	A60131	G86053	E91207	B65171	AI3056	E98229	ID
hypothetical prote		conserved hypothet		cal		alpha-2-macroglobu	alpha-2-macroglobu	alpha-2-macroglobu	cyclin G-associate	ISGF3 p91-related	hypothetical prote	conserved hypothet		hypothetical prote		glycerol-3-P dehyd	conserved hypothet			hypothetical prote	transcription fact	hypothetical prote		•		•	sarcosine oxidase	sarcosine oxidase	Description

sarcosine oxidase gamma subunit [imported] - Agrobacterium tumefaciens (strain C58, D C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002 C; Accession: AI3056 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A; Accession: AI3056 A; Accession: AI30577; PMID:11743193 A; Accession: AI3058 A; Scatus: preliminary A. Molecule Tone. DNA

A;Molecule type: DNA A;Residues: 1-184 <KUR> A;Cross-references: GB:AE008689; PIDN:AAL44871.1; PID:917742519; GSPDB:GN00187 A;Experimental source: strain C58 (Dupont) C;Genetics: A;Gene: soxG

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T18534 B84683	JH0796 S76549	A43920	S71508 B83052	809500 883818	в95060 G97928	S39342	I39837
protein-tyrosine k hypothetical prote	nucleolar 100K pol transcription-repa	hypothetical prote nucleolar 100K pol	dnak-type molecula Dnak protein PA476	dnak-type molecula class I heat-shock	dnaK protein [impo hypothetical prote	dnak-type molecula	-type mol

ALIGNMENTS

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RESULT
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C; Superfamily: 1
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A; Residues: 1-416 <HAY>
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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
Lle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7
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C;Accession: E91207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein ECs4629 [imported] - Escherichia coli (strain 0157:H7, substrain
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C:Superfamily: Escherichia coli hypothetical protein yidR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE000446; GB:U00096; NID:g2367261; PIDN:AAC76712.1; PID:g1790124 A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein yidR - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-416 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; nucleic acid sequence not shown; translation not
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; B.

Rose, D.J.; Mau, B.; Shao, Y.

nce 277, 1453-1462, 1997

Le: The complete genome sequence of Escherichia coli K-12.

Ference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                               atus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                       erence number: A99629; MUID:21156231; PMID:11258796
ession: E91207
                                                           272 LPAPPRGIVQRRLTF 286
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8; Conserv
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8; Conserv
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Corynebacterium sp.
                                                                                                                                               Conservative
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                                                                                                                                                                 53.2%;
46.7%;
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                                                                                                                                                                 Score 41; DB Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42;
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2; Mismatches
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Pred. No.
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                                                                                                                                                                                     Length 416;
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  R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.(
                                                                  C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                  C; Accession:
                                                                                            C; Species: Halobacterium sp. NRC-
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                                                                                                                                                                                                                                                                  Qy
                                                                                                                hypothetical protein Vng1564h [imported] - Halobacterium sp.
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Lasky G.; Ja

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C;Keywords: DNA binding; homeobox; nucleu: F;171-227/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X58773

R;Su, M.W.; Suzuki, R.H.; Solursh, M.; Ramirez, F.
submitted to the EMBL Data Library, December 1990
A;Reference number: S14513

A;Accession: S14513
                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-295 <SUA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homeotic protein Xhox-7.1 - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 24-Sep-1999
C;Accession: A60131; S14513
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A; Residues: 2-295 <SUA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Progressively restricted expression of a new homeobox-containing gene during A;Reference number: A60131; MUID:91347929; PMID:1679007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Su, M.W.; Suzuki, H.R.; Solursh, M.; Ramirez, Development 111, 1179-1187, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G86053
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE005174; NID:g12518530; PIDN:AAG58891.1; A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-416 <STO>
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                                                                                           Matches
                                                                                                                                    Query Match
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275 LPMSPMGLYTAHLGY
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                                                                                                             Similarity
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                                                                                                         51.98;
46.78;
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46.7%;
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                                                                                                         Score 40; DB Pred. No. 19;
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Pred. No.
                                                                                      Mismatches
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18;
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E.; Potamousis, K.;
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Apoda
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R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, ; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, (A.;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi: A.;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: A64339
                                                                                                                              A;Cross-references: GB:U67486; GB:L77117; NID:g1591031; PIDN:AAB98309.1; PID:g1592281;
                                                                                                                                                                                                                   A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein mJ0312 - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Decies: Methanococcus jannaschii C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C;Accession: A64339
                                                                                             A; Map position: REV291845-291225
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C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keyvords: DNA binding; homeobox; nucleus; transcription regu
F;1-45/Domain: homeobox homology (fragment) <HOX>
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C;Genetics:
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A; Residues: 1-113 <SIM>
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A;Title: Differential expression of myogenic regulatory genes and Msx-1 during dediffere A;Reference number: IS1024; MUID:95218226; PMID:7703517
A;Accession: IS1025
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C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Sep-1999
C;Accession: I51025
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A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84309
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A; Residues: 1-407 <STO>
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                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>.</u>,
                                 Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40;
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                           DB 2;
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9.6;
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                           Length 206;
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conserved hypothetical protein SMa2361 [imported] - Sinorhizobium meliloti (strain 10
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                              RESULT 12
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                                                                                                      E95421
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C; Superfamily: Enterobacter ribonuclease
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                                                                                                                                                                                                                                                                                  A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                 A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vol.; Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.;Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribonuclease homolog HI0526 - Haemophilus influenzae (strain Rd KW20) C;Species: Haemophilus influenzae (c;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                           A; Residues: 1-272 <TIGR>
                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                         A; Accession: C64009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 17q21-17q21
C; Superfamily: human signal transducer and transcription activator STAT5A
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A:Accession: A54444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:L29277; NID:g475788; PID:g475789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-770 < RES>
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C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 28-Jul-2000
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                                                                                                       Matches
                                                                                                                                                      Query Match
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                                                                                                                                                                                                  Cross_references: GB:U32735; GB:L42023; NID:g1573509; PIDN:AAC22192.1; PID:g1573510
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170 DLPALPKGLLAQYL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   723 DLPMSPRAL 731
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                                                                                                                            Local Similarity
                                                 1 DLPMSPRGVIASNL 14
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77.8%;
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                                                                                                                    Score 38; DE
Pred. No. 39;
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7; Mismatches
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                                                                                                                                         Length 272;
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#sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

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A; Experimental source: strain 1021, megaplasmid pSymA
R; Galibert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Fitle: The composite genome of the legume symbiont Sinorhizobium meliloti.
A.Reference number: A96039; MUID:21368234; PMID:11474104
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R;Barnett, M.J; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows, R;Barnett, M.J; Fisher, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: E95421
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A; Residues: 1-328 <KUR>
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                                                                                         glycerol-3-phosphate dehydrogenase, NAD-dependent CP1014 [imported] - Chlamydophila pneu C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000 C;Accession: G72024; D81513
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A; Residues: 1-334 <STO>
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A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis A; Reference number: A72000; MUID:99206606; PMID:10192388
                                           R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain J138
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he: SMa2361
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erfamily: glycerol-3-phosphate dehydrogenase
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9; Conser
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB Pred. No. 50;
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A; Residues: 1-334 < REA>
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A; Residues: 1-334 <ARN>
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               hypothetical protein B1937_C3_231 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 22-Oct-1999
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A; Residues: 1-363 < CAR>
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                                                                                                                                                                                     183 MPVKKKGVVKSNYAF 197
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                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                    2 LPMSPRGVIASNLXF 16
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                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                              49.4%;
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A;Experimental source: strain CWLO29
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
A;Pitle: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: D81513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein - Autographa californica nuclear polyhedrosis virus C; Species: Autographa californica nuclear polyhedrosis virus, AcMNPV A; Note: dsDNA virus virus, AcMNPV C; Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 21-Jul-2000 C; Accession: G72854; A45684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: gpdA; CF1V14
C;Superfamily: glycerol-3-phosphate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: G72024
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D. Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis vir A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Accession: G72854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE002258; GB:AE002161; NID:g7189919; PIDN:AAF38792.1; PID:g718
A;Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                   R;Carstens, E.B.; LU, A.L.; Chan, H.L.
J. Virol. 67, 2513-2520, 1993
A;Title: Sequence, transcriptional mapping, and overexpression of p47, a baculovirus A;Reference number: A45684; MUID:93233214; PMID:8474157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:L22858; NID:g510708; PIDN:AAA66669.1; PID:g559108 R;Carstens, E.B.; Lu, A.L.; Chan, H.L.
                                                                                                                                                                                               A;Cross-references: GB:L07878; NID:g293990; PIDN:AAA16858.1; PID:g293991
A;Note: sequence extracted from NCBI backbone (NCBIN:129587, NCBIP:129588)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.4%; Score 38; DE 50.0%; Pred. No. 50;
                              Score 38; DE Pred. No. 54;
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Mismatches
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                                                                 Length 363;
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C; Accession: 690473

R; She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Char Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
          A;Gene: cutA-6
C;Superfamily: carbon-monoxide dehydrogenase large chain
                                                                      A;Cross-references: GB:AE006641; NID:gl3816315; PIDN:AAK43046.1; GSPDB:GN00155 C;Genetics:
                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-684 <KUR>
                                                                                                                                                                                                                                                                                                                                                               hypothetical protein cutA-6 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-Aug-2001
                                                                                                                                                                                    A;Reference number: A99139
A;Accession: G90473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE001886; GB:AE000513; NID:g6457921; PIDN:AAF09837.1; PID:g645792
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-670 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein - Deinococcus radiodurans (strain R1) C;Species: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S72582
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Reference number: S72580
A;Accession: S72582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-479 <SMI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U00016; NID:g466961; PIDN:AAA17150.1; PID:g466964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 SPRGVIASNLXF 16
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Pred. No. 1.1e+02;
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Pred. No.
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1015 DLPAEPNKVIASS 1027
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A; Molecule type: mRNA
A; Residues: 1-1305 < KAN>
A; Cross-references: EMBL: D38560; NID: 91902912; PIDN: BAA18911.1; PID: 91902913
                                                                                                                                                                                                                                                                                                                                                                                                                   C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C:Accession: T31096
                                                                                                                                               A; Gene: GAK
                                                                                                                                                                                                                                                                                                                  A;Title: GAK: a cyclin G-associated kinase contains a tensin/auxilin-like domain.
A;Reference number: Z20979; MUID:97165969; PMID:9013862
A;Accession: T31096
                                                                                                                                                                                       A; Note: GAK and cyclin G associate together in vivo
                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                             R;Kanaoka, Y.; Kimura, S.H.; Okazaki, I.; Ikeda, M.; Nojima, H. FEBS Lett. 402, 73-80, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-393,'M',395-700,702-770 <RE2>
A:Cross-references: EMBL:U08378; NID:g473889; PIDN:AAA56668.1; PID:g473890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Acute phase response factor and additional members of the interferon-stimula A;Reference number: 149009; MUID:95014185; PMID:7523373
A;Accession: 149009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:L29278; NID:g476715; PIDN:AAA37254.1; PID:g476716
R;Raz, R.; Durbin, J.E.; Levy, D.E.
J. Biol. Chem. 269, 24391-24395, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 01-Dec-2000
C;Accession: I49508; I49009
R;Akira;S; Nishio, Y; Inoue, M.; Wang, X.J.; Wei, S.; Matsusaka, T.; Yoshida, K.;
Cell 77, 63-71, 1994
A;Title: Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-related A;Reference number: A54444; MUID:94208062; PMID:7512451
A;Accession: I49508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cyclin G-associated kinase GAK - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: human signal transducer and transcription activator STATSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-770 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                 Query Match
                                                                                                                                                                           Genetics:
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                                                                       Local Similarity
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1 DLPMSPRGVIASN 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DLPMSPR 7
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                                                Conservative
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                                                               49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.4%; Score 38; DB 2; 100.0%; Pred. No. 1.3e+(
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                                                                  Score 38; I
Pred. No. 2
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Pred. No. 1.1e+02;
"'amatches 1;
                                             Mismatches
                                                                                         DB 2;
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                                                                  3e+02;
                                                                                      Length 1305;
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                                      Indels
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Search completed: January 2, 2003, 12:04:49 Job time : 18 secs

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OM protein - protein search, using sw model
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January 2, 2003, 12:03:00 ; Search time 32 Seconds (without alignments) 20.738 Million cell updates/sec
                                                                                                                                                               GenCore version 5.1.3 Compugen Ltd.
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Title: Perfect score: Sequence:

US-09-824-053-3 77 1 DLPMSPRGVIASNLXF 16

ing table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

rched:

112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ŭ	. U.	31	30	29	28	27	26	ຸນ	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ر. د	4	ω	N	۲	Result No.
3/	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	38	38	38	38	38	38	38	38	38	39	39	40	42	Score
48.1	. 8		.8	8	8		8	8	.8		8	8	8			48.1	8	8	8	9	49.4	9	49.4	49.4	49.4	49.4	49.4	49.4	50.6	•	۲	54.5	Query
1199	887	885	861	656	644	637	613	613	610	610	609	607	607	607	606	604	500	499	196	4544	4543	1305	770	770	590	363	334	272	770	206	295	416	Length
۲	ш	-	<u>سر</u>	ب	۲	Ь	Н	_	۳	<u>, .</u>	<u>, , , , , , , , , , , , , , , , , , , </u>	Н	Н	_	_	_			۳											-	1	1	DB
MED_SYNY3	PMC2_MOUSE	PMC2_HUMAN	ORC1_HUMAN	DNAK_COXBU	DNAK_LEGPN	DNAK_PSEAE	DNAK_LACSK	DNAK_BACHD	DNAK_BACSU	DNAK_BACSH	DNAK_STRAG	DNAK_STRPY	DNAK_STRPN	DNAK_LACLA	DNAK_BACTR	DNAK_BACME	GGPS_PSEAG	GAK_MOUSE	FLC_ARATH	LRP1_HUMAN	LRP1_CHICK	GAK_RAT	STA3_RAT	STA3_MOUSE	DNAK_STRMU	VP43_NPVAC	GPDA_CHLPN		STA3_HUMAN	2	HX71_XENLA	YIDR_ECOLI	ID
Q55750 synechocyst	mus m	homo	homo sapi	2 coxiella	legionella	3 pseudomo	7 lactobaci	bacillus	0 bacillus s	æ	ω			lactococc	bacillus	P05646 bacillus me	pse		7 arabi	4 homo sa	gallus	rattus		mus muscul		autographa		N	homo sapie	0 methano		cheri	Š

5	44	43	42	41	40	39	38	37	36	. U	34
36	36	36	36	36	36	36	36.5	37	37	37	37
46.8	46.8	46.8	46.8	46.8	46.8	46.8	47.4	48.1	48.1	48.1	48.1
421	409	388	349	297	269	158	293	1493	1477	1461	1377
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Y118_TREPA	YOPM_YERPE	AMPC_YEREN	LDH_ALCEU	PECM_ERWCH	NUDC_VIBCH	YC76_MYCTU	Y698_CHLMU	NEO1_MOUSE	HTK7_HYDAT	NEO1_HUMAN	NEO1_RAT
083155 treponema p		P45460 yersinia en									

ALIGNMENTS

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RESULT HX71_X ID H AC Q DT 0 DT 0 DT 1 DT 1 DC H CGN XX OC E	DR DR KW SQ Qu Bee Ma Db	# 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	RESULT YIDR_E ID Y AC P AC P DT 1 DT 1 DT 1 DT 1 CON P C CON P C CON P C C C C C C C C C C C C C C C C C C C
LIT 2 _XENLA _X	EMBL; AE000446; AAC76712.1; -: ECOGene; EG1113; yidr. ECOGene; EG11713; yidr. Hypothetical protein; Complete proteome. SEQUENCE 416 AA; 46318 MW; 47E36360CC89ABB7 CRC64; Query Match S4.5%; Score 42; DB 1; Length 416; Best Local Similarity 53.3%; Pred. No. 4.9; Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0; 2 LPMSPRGVIASNLXF 16	SEQUENCE FROM N.A. STRAIN-KI2 / MG1655; MEDLINE-9315143; PubMed-7686882; BUTLINE-9315143; PubMedt G. III, Daniels D.L., Blattner F.R.; BUTLINE-9315143; PubMedt G. III, Daniels D.L., Blattner F.R.; BUTLINE-9315141; PumKett G. III, Daniels D.L., Blattner F.R.; BUTLINE-9315141; PumKett G. III, Daniels D.L., Blattner F.R.; BUTLINE-9315141; PumMetry around the origin of replication."; Genomics 16:551-561(1993). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/orsend an email to license@isb-sib.ch). EMBL; L10328; AAA62041.1;	LT 1 ECOLI STANDARD; PRT; 416 AA. P31455; P76734; 01-JUL-1993 (Rel. 26, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-2002 (Rel. 41, Last annotation update) Hypothetical protein yidk. YIDR OR B3689. Escherichia coli. Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia. NCBL_TaxID=562;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y312_METJA STANDARD; PR Q55756; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last seque 16-OCT-2001 (Rel. 40, Last annot Hypothetical protein MJ0312.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDILINE-9637999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00389; HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene during Xenopus laevis embryogenesis.";
DeveLopment 111:119-1187(1991).
-i- SUBCELLULAR LOCATION: Nuclear (Probable).
-i- DEVELOPMENTAL STACE: APPEARS AT THE BEGINNING C
PLATEAU BETWEEN THE NEURULA AND MIDDLE-TAILBUD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91347929; PubMed=1679007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Su M.-W., Suzuki H.R., Solursh M., Ramirez F.;
"Progressively restricted expression of a new homeobox-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homeobox; DNA-binding; Developmental protein; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DECREASE STEADILY THEREAFTER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170
295 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanocaldococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMEOBOX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              054331E2BC106C10 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF GASTRULATION
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RESULT 4
STA3_HUMAN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STA3_HUMAN
P40763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Complete proteome. SEQUENCE 206 AA; 22367 MW; 1168AB576BFE033A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             jannaschii.";
Science 273:1058-1073(1996).
                                                                                                                                                                                                            -i- PATHWAY: INVOLVED IN THE GP130-MEDIATED SIGNALING PATHWAY.
-i- SUBUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH A RELATED FAMILY MEMBER (AT LEAST STATL).
                                                                                                                                                                                                                                                                                                                                                                         pHOSPHORYLATION ON SERINE.

MEDLLNE-95215843; PubMed-7701321;

Zhang X., Blenis J., Li H.-C., Schindler C., Chen-Kiang S.;

"Requirement of serine phosphorylation for formation of STAT-promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Akira S., Nishio Y., Inoue M., Wang X.-J., Wei S., Matsusaka T., Yoshida K., Sudo T., Naruto M., Kishimoto T., Yoshida K., Sudo T., Naruto M., Kishimoto T., "Molecular cloning of APBR, a novel IFN-stimulated gene factor 3 p91-related transcription factor involved in the gp130-mediated signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       response factor).
STAT3 OR APRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal transducer and activator of transcription 3 (Acute-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR; MJ0312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U67486; AAB98309.1; -.
                                                                                                                                                                                                                                                                        -i- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS (IL-6)-RESPONSIVE ELEMENTS IDENTIFIED IN TACUTE-PHASE PROTEIN GENES.
                                                                                                                                                                                                                                                                                                                                        Science 267:1990-1994(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94208062; PubMed=7512451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DLPMSPRGVIASNL 14
                                                                                      response to phosphorylation.
TISSUE SPECIFICITY: HEART, BRAIN, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, AND PANCREAS.
PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-6, IL-11, CNTF, PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-6, IL-11, CNTF, PTM: TYROSINE PHOSPHORYLATION AND OSM. SERINE PHOSPHORYLATION
                HOMODIMERS AND MAXIMAL TRANSCRIPTIONAL ACTIVITY.
SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS
SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear; translocated into the nucleus in
                                                                          LIF, CSF-1, EGF, PDGF, IFN-ALPHA AND OSM. SERINE PHOSIS IMPORTANT FOR THE FORMATION OF STABLE DNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77:63-71(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.6%;
35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; I
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               770 AA
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                                                                                                                                                                                                                                                                                                                 TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 206;
                                                                                                                                                                                                                                                                                                 THE INTERLEUKIN-6
PROMOTERS OF VARIOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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CCCCCCTTTA RANGER RANGE
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InterPro: IPR001217; STAT.
Pfam; PP00017; SH2; 1.
Pfam; PF01017; STAT; 1.
Pfam; PF02864; STAT_Dind; 1.
Pfam; PF02865; STAT_Drot; 1.
SMART; SM00252; SH2; 1.
                                                                                                                                                                                                                                                                                                        MEDLINE-95350630; PubMed-7542800;
Flelschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shriley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                                                                                                                                                                                                                                                                     Fine L.D., Fritchman J.L.,
Gnehm C.L., McDonald L.A.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-Rd / KW20 / ATCC 51907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Haemophilus.
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01-NOV-1995 (Rel.
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TRANSEAC; T01493; -. Genew; HGNC:11364; STAT3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae
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15-JUN-2002 (Rel.
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Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                 Science 269:496-512(1995).
-!- SIMILARITY: BELONGS TO THE RNASE T2 FAMILY.
                                                                                                                                                                                                                                                                         "Whole-genome random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probable ribonuclease HI0526
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7; Conser
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727
770 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32, Created)
32, Last sequence update)
41, Last annotation update)
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77.8%;
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                                                                                                                                                                                                                                                                      sequencing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma subdivision; Pasteurellaceae;
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Pred. No.
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                                                                                                                                                                                                                                                                      assembly
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                                                                                                                                                                                                                                                                      of.
   Usage
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      commercial
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RESULT 6
GPDA_CHLPN
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Best Local
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    Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).

-!- CATALYTIC ACTUVITY: Sn-glycerol 3-phosphate + NAD(P)(+) = glycerone phosphate + NAD(P)H.

-PATHWAY: De novo phospholipid biosynthesis; glycerol-3 phosphate
                                                                                                                                                                                                       White O., Hickey E.K., Peterson J., Utterback T., Berry K., B. Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzbeisen J., Fraser C.M.;
"Genome secures C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glycerol-3-phosphate dehydrogenase (NAD(P)+)
dependent glycerol-3-phosphate dehydrogenase)
GPSA OR GPDA OR CPN0855 OR CP1014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPDA_CHLPN
Q9Z751;
                                                                                       MEDLINE-20330349; PubMed-10871362;
Shirai M., Hirakawa H., Kimoto M., Tabu
Shiba T., Ishii K., Hattori M., Kuhara
                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99206606; PubMed-10192388;
Kalman S., Mitchell W., Marathe R., Lammel C.,
Olinger L., Grimwood J., Davis R.W., Stephens F
                                                                                                                                                                                     "Genome sequences of Chlamydia trachomatis MoPn and pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00530; RNASE_T2_1; PROSITE; PS00531; RNASE_T2_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                         Nucleic Acids Res.
                                                                                                                                                                                                                                                                                 MEDLINE=20150255; PubMed=10684935;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     "Comparative
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                                                                                                                                                SEQUENCE FROM N.A.
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195
199
272
                                                                                                                                                                                                                                                                                                                                                Grimwood J., Davis R.W., Stephens R.S.; e genomes of Chlamydia pneumoniae and C. trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; Hydrolase; Nuclease; Endonuclease; Signal;
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272
148
195
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31482
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PROBABLE RIBONL
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred. No.
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. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 272;
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Salzberg
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RESULT 7
VP43_NPVAC
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Best Local
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                                                                                                                                                                                                                                                                                                                J. Virol. 67
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01-FEB-1994
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERM; PFO1210; NAD_Gly3P_dh; 1.
PERM; PF01210; ORD Gly3P_dh; 1.
PRONTS; PR00077; GPDHDRGNASE.
PROSITE; PR00057; NAD_G3PDH; 1.
PROSITE; PR00057; NAD_G3PDH; 1.
PROSPHOLLPID BLOSYNTHESIS; Oxidored SEQUENCE 334 AA; 36161 MW; 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
              EMBL;
                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Autographa californica nuclear polyhedrosis virus (AcMNPV). Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus.
                                                                                                                                                                                         polyhedrosis virus.";
Virology 202:586-605(1994).
                                                                                                                                                                                                                     "The complete DNA sequence of Autographa californica nuclear nolyhedrocic virus ":
                                                                                                                                                                                                                                              MEDLINE=94303173; PubMed=8030224;
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
                                                                                                                                                                                                                                                                                 STRAIN-C6
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   "Sequence, transcriptional mapping, and overexpress baculovirus gene regulating late gene expression.";
J. Virol. 67:2513-2520(1993).
                                                                                                                                                                                                                                                                                                                                                                                      Carstens E.B., Lu A.L., Chan H.L.B.;
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93233214; PubMed=8474157;
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-HR3
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable)
-!- SIMILARITY: BELONGS TO THE NAD-DEPENDENT GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=46015;
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nes 7; Conserv
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 L07878;
L22858;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 32, Last annotation updat
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 AAA16858.1;
AAA66669.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; AAD18993.1; -.; AAF38792.1; -.; BAA99063.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ithesis; Oxidoreductase; NAD; Complete proteome.
36161 MW; 4339ED6FFD77CEE6 CRC64;
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STA3_MOUSE
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Best Local Similarity
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chaperone protein dnaK (Heat shock protein 70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jayaraman G.C., Penders J.E., Burne R.A.; "Transcriptional analysis of the Streptococcus mutans hrca, grpE and dnaK genes and regulation of expression in response to heat shock and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97426041; PubMed=9282745;
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                                                                                                                                                               432 DIPAAPRGVPQIEVTF 447
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                                                                                                                                                                                                                 \mathbf{L}
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FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY)
INDUCTION: BY HEAT SHOCK
INDUCTION: BY HEAT SHOCK PROTEIN
                                                                                                                                                                                                                 DLPMSPRGVIASNLXF 16
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Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
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                           770 AA
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                                                                                                                                                                                                                                                                                                                      1; Length 590;
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RRR ROCCOS GE DOT
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     -I- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE INTERLEUKIN-6
(IL-6)-RESPONSIVE ELEMENTS IDENTIFIED IN THE PROMOTERS OF VARIOUS
ACUTE-PHASE PROTEIN GENES. STAT3B INTERACTS WITH THE N-TERMINAL
PART OF C-JUN TO ACTIVATE SUCH PROMOTERS IN A COOPERATIVE WAY.
-I- PATHWAY: INVOLVED IN THE GP130-MEDIATED SIGNALING PATHWAY.
-I- SUBUNIT: FORMS A HOMODIMER OR A HETERODIMER WITH A RELATED FAMILY
MEMBER (AT LEAST STAT1) (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: Nuclear; translocated into the nucleus in
response to phosphorylation.
-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; STAT3A (SHOWN HERE) AND STAT3B;
ARE PRODUCED BY ALTERNATIVE SPLICING.
-I- TISSUE SPECIFICITY: STAT3A IS SEEN IN THE LIVER, SPLEEN, AND
KIDNEY. STAT3B IS ALSO DETECTED IN THE LIVER, ALTHOUGH IN A MUCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94188718; PubMed-8140422; Zhong Z., Wen Z., Darnell J.E. Jr.; "Stat3: a STAY featily member activated by tyrosine phosphorylation response to epidermal growth factor and interleukin-6."; Science 264:95-98(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathway.";
Cell 77:63-71(1994).
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MEDLINE-94208062; PubMed-7512451;

Akira S., Nishio Y., Inoue M., Wang X.J., Shi W., Matsusaka T.,

Yoshida K., Sudo T., Naruto M., Kishimoto T.;

Molecular cloning of APRF, a novel IFN-stimulated gene factor 3 p91-

Telated transcription factor involved in the gpl30-mediated signaling

Teathery T.
                                                                                                                                                                                                                                                   Nature 394:145-151(1998).
                                                                                                                                                                                                                                                                                   MEDLINE-98334373; pubMed-9671298; Becker S., Groner B., Mueller C.W.; "Three-dimensional structure of the
                                                                                                                                                                                                                                                                                                                                                                                       Wen Z., Zhong Z., Darnell J.E. Jr.;
"Maximal activation of transcription by Statl and
tyrosine and serine phosphorylation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION OF SER-727, AND MEDLINE-95354205; PubMed-7543024;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STAT3 OR APRF.
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Signal transducer
                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 136-716
                                                                                                                                                                                                                                                                                                                                                                            Cell 82:241-250(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Acute phase response factor and additional members of the interferon-stimulated gene factor 3 family integrate diverse signals from cytokines, interferons, and growth factors.";
J. Biol. Chem. 269:24391-24395(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R., Durbin J.E., Levy D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natl. Acad.
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34,
MANNER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last anotation update)
activator of transcription 3 (Acute-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND MUTAGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nathans D.; activity of Jun and Stat3 beta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                   Stat3beta homodimer bound
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RESULT 10

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ID STA3_RAT STAN

AC P52631;

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DT 01-CCT-1996 (Rel. 3

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Best Local
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InterPro; IPR000980; SH2.
InterPro; IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01017; SH2; 1.
Pfam; PF02864; STAT_brot; 1.
Pfam; PF02865; STAT_prot; 1.
SMART; SM00252; SH2; 1.
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EMBL; U06922;
EMBL; U08378;
EMBL; U30709;
PDB; 1BG1; 13-
                                                                                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                             VARIANT
MUTAGEN
                                                                     Eukaryota;
Mammalia; E
                                                                                                       STAT3
                                                                                                              Signal transducer and activator of transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restues by non-profit institutions as long as its content
 Ripperger
           MEDLINE-96102059; PubMed-8530402;
                                                                                           Rattus norvegicus
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
                        rissuE=Liver;
                                   SEQUENCE FROM N.A.
                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFAC;
                                                                                                                                                                                                                              723
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                   1 DLPMSPR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-6, IL-11, CNTF, LIF, CSF-1, EGF, PDGF, IFN-ALPHA AND OSM. SERINE PHOSPHORYLATION IS IMPORTANT FOR THE FORMATION OF STABLE DNA-BINDING STAT3 HOWODINERS AND MAXIMAL TRANSCRIPTIONAL ACTIVITY (BY SIMILARITY). SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS. SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                             DLPMSPR 729
                                                                                                                                                                                                                                                                                     Similarity
                                                                     Eutheria;
                                                                              Metazoa;
                                                                                                                                                                                                                                                                                                                       770
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          580
705
727
716
                                                                                                                                                                                                                                                                                                                                                                             701
727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; AAA37254.1; -.; AAA19452.1; -.; AAA56668.1; -.; AAC52612.1; -.
                                                                                                                                                                                                                                                                                                                                              16
25
                                                                                                                                                                                                                                                                                                                       A
A
                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative
                                                                                                                           41,
                                                                                                                                    34, Created)
34, Last seq
                                                                                         (Rat).
                                                                                                                                                                                                                                                                                                                                  394
                                                                                                                                                                                                                                                                                                                                                                             701
727
                                                                     Rodentia;
                                                                             Chordata;
                                                                                                                                                                                                                                                                                                                                              16
25
                                                                                                                                                                                                                                                                                                                       88053 MW;
                                                                                                                                                                                                                                                                                     100.0%;
 :
:
                                                                                                                                                                                                                                                                                                 49.48;
                                                                                                                         Last sequence update)
Last annotation update)
   Richter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding;
lve splicing;
                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                    Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                              ACTIVATION.
E -> K (IN I
S -> T (IN I
M -> I (IN I
                                                                                                                                                                                                                                                                                                                                                                             MISSING
S->A: DE
                                                                                                                                                                                                                                                                                                                                                                                                              FDMDLTSECATSPM ->
                                                                                                                                                                                                                                                                                                                                                                                                                         TTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQFESLT
                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION
                                                                  Sciurognathi;
                                                                              Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                     6C00626711C8012D CRC64;
                                                                                                                                                                                                                                                                          Mismatches
×.
                                                                                                                                                                                                                                                                                                                                                                             DECREASED
                                                                                                                                                                                                                                                                                                                                                                                         (IN SOME CLONES)
                                                                                                                                                                      770 AA.
  Hocke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear protein; 3D-structure.
                                                                                                                                                                                                                                                                                    DB 1;
51;
                                                                                                                                                                                                                                                                                                                                 REF.
                                                                                                                                                                                                                                                                                                                                                      REF.
 G
                                                                   Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY
                                                                                                                                                                                                                                                                                                                                                                             TRANSCRIPTIONAL
 .M., Lottspeich
                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                              Length 770
                                                                                                                                                                                                                                                                                                                                          AND 4).
                                                                                                                                                                                                                                                                                                                                                                                                              FIDAVWK
                                                                                                                                                                                                                                                                                                                                                                                                                                              JAK)
                                                                                                                                                                                                                                                                         Indels
                                                                  Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
                                                                                                                                                                                                                                                                                                                                                                                                             (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration -
                                                                                                                                                                                                                                                                        0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  outstation
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RA RA
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FTT
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CC -!- FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE INTERLEUKIN-6

CC (II-6)-RESPONSIVE ELEMENTS IDENTIFIED IN THE PROMOTERS OF VARIOUS

CC ACCUTE-PHASE PROTEIN GENES.

CC -!- PATHWAY: INVOLVED IN THE GP130-MEDIATED SIGNALING PATHWAY.

CC -!- PATHWAY: INVOLVED IN THE GP130-MEDIATED SIGNALING PATHWAY.

CC -!- SUBCULULAR LOCATION: Nuclear: translocated into the nucleus in

CC -!- SUBCELLULAR LOCATION: Nuclear: translocated into the nucleus in

CC response to phosphorylation (By similarity).

CC -!- PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-6, IL-11, CNTF,

CC -PTM: TYROSINE PHOSPHORYLATED IN RESPONSE TO IL-6, IL-11, CNTF,

CC IS IMPORTANT FOR THE FORMATION OF STALES DNA-BINDING STATIS

CC -- SIMILARITY: BELONGS TO THE STAT FAMILY OF TRANSCRIPTION FACTORS.

CC -- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
TISSUE-Kidney;
MEDLINE-97165969; PubMed-9013862;
Kanaoka Y., Kimura S.H., Okazaki I., Ikeda M., Nojima H.;
"^"" a rurlin G associated kinase contains a tensin/auxilin-like
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR000980; SH2.
InterPro: IPR001217; STAT.
Pfam; PF00017; SH2; 1.
Pfam; PF01011; STAT; 1.
Pfam; PF02864; STAT_bind; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50001; SH2; 1.
Transcription regulation; DNA-binding; Nuclear protein;
Phosphorylation; SH2 domain. ...
                                                                                                                                                                                                                                                                                                                                                                                         723 DLPMSPR 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF02865; STAT_prot; 1.
SMART; SM00252; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/profit institutions and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X91810; CAA62920.1; -. HSSP; P42227; 1BG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW
                                                                                                                                                                                                                                                                                                                                                                                                                            1 DLPMSPR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poca 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nuclei late in an acute phase response and bind interleukin-6 response elements.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fey G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription factors Stat3 and Stat5b are present in rat liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         727
770 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.4%; Score 38;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY JAK)
PHOSPHORYLATION (BY SIMIL)
D74A0C76954754ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY JAK) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 770;
                                                                                                                                   Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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LRP1
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                                                                                                                                                                                                                                                                                                                                     Ωy
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
STRAIN-White leghorn; TISSUE-Liver, and Ovary; MEDLINE-94103212; PubMed-7506255; Nimpf J., Stifani S., Bilous P.T., Schneider W.J.;
                                                                                                                                           LRP1_CHICK STANDARD; PRT; 4543 AA.

P98157;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Low-density lipoprotein receptor-related protein 1 precursor (LRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IFR000340; DS_phosphatase.
InterPro; IFR0001623; DnaJ_N.
InterPro; IFR000719; Euk_pkinase.
InterPro; IFR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PF000256; DnaJ; 1.
ProDom; PF00001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                       CHICK
                                                     SEQUENCE FROM N.A.
                                                                               NCBI_TaxID=9031;
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                             (Alpha-2-macroglobulin receptor) (A2MR). Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                    1015 DLPAEPNKVIASS 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein; Endoplasmic reticulum; Cell DOMAIN 40 315 PROTEIN KINASE. 173 173 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00107; PROTEIN KINASE_ATP; FALSE_NEG. PROSITE; PS00108; PROTEIN KINASE_ST; 1. PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. PROSITE; PS00636; DNAJ_1; FALSE_NEG. PROSITE; PS50076; DNAJ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00271; DnaJ; 1.
SMART; SM00012; PTPC_DSPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D38560; BAA18911.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trans-Golgi network. Also seen on the plasma membrane, probably focals adhesions (By similarity).

-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-!- SIMILARITY: CONTAINS 1 TENSIN DOMAIN.
                                                                                                                                                                                                                                                                                                                              1 DLPMSPRGVIASN 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>'</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain.";
FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Associates with cyclin G and CDK5. Seems to act as an auxilin homolog that is involved in the uncoating of clathrin-coated vesicles by Hsc70 in non-neuronal cells. Expression oscillates slightly during the cell cycle, peaking at G1 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Localizes to the perinuclear area and
                                                                                                                                                                                                                                                                                                                                                             Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                 \frac{1241}{1305}
                                                                                                                                                                                                                                                                                                                                                                                                                                             40
173
405
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402:73-80(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                       Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                             689
1305
                                                                                                                                                                                                                                                                                                                                                                     49.4%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                           143702 MW;
                                                                                                                                                                                                                                                                                                                                                                  Score 38;
Pred. No.
                                                                                                 Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                          J-DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          TENSIN
                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    6D36BD38011C44EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                            Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cycle
                                                                                                                                                                                                                                                                                                                                                                            Length 1305;
                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                           Gaps
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      TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                   PROSITE; PS00010; ASX_HYDROXYL; 3
PROSITE; PS00022; EGF_1; 5.
PROSITE; PS01186; EGF_2; 7.
PROSITE; PS01187; EGF_CA; 2.
PROSITE; PS01209; LDLRA_1; 27.
PROSITE; PS01209; LDLRA_2; 31.
                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00058; Id.
PRINTS; PR00010; I
PRINTS; PR00261;
PRINTS; SM00179; EC
SMART; SM00192; EC
SMART; SM00192; EC
SMART; SM00192; EC
SMART; SM001935; L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPRO00152; A
InterPro; IPRO00561; E
InterPro; IPRO01881; E
InterPro; IPRO01438; E
InterPro; IPRO02172; L
InterPro; IPRO002172; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                Receptor; Transmembrane; Signal; Calcium-binding; Alternative splicing.
                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>-</u> .
                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X74904; CAA52870.1; -. HSSP; Q07954; 1CR8.
                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The somatic cell-specific low density lipoprotein receptor-related protein of the chicken. Close kinship to mammalian low density lipoprotein receptor gene family members.";

J. Biol. Chem. 269:212-219(1994).

-I- FUNCTION: INVOLVED IN THE PLASMA CLEARANCE OF CHYLOMICRON REMNANTS AND ACTIVATED ALPHA 2-MACROGLOBULIN, AS WELL AS THE LOCAL METABOLISM OF COMPLEXES BETWEEN PLASMINGGEN ACTIVATORS AND THEIR ENDOCENOUS INHIBITORS. BINDS VITELLOGENIN, CALCIUM AND ALPHA 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MACROGLOBULIN.

SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are

produced by alternative splicing.

TISSUE SPECIFICITY: SOMATIC.

PTM: CLEAVED INTO A 85 KDA MEMBRANE-SPANNING SUBUNIT (LRP-85) AND

A 515 KDA LARGE EXTRACELLULAR DOMAIN (LRP-515) THAT REMAINS NON-

COVALENTLY ASSOCIATED.

SIMILARITY: CONTAINS 31 LDL-RECEPTOR CLASS A DOMAINS.

SIMILARITY: CONTAINS 31 LDL-RECEPTOR CLASS A DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00008; EGF; 14.
PF00057; ldl_recept_a; 31.
PF00058; ldl_recept_b; 33.
         44420
44444
72
72
113
152
476
891
895
895
932
932
1011
1058
1100
                                                                                                                                                                                                                                                               splicing
                                                                                                                                                                                                                                                                                                                                                                                EGF_CA; 3.
EGF_like; 18.
LDLa; 31.
LY; 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGFBLOOD.
                                                                                                                                                                                                                                        21
4543
                                                                                                                                                                         4419
4443
4543
68
         112
151
191
522
841
890
931
1011
1011
1051
1097
1105
1105
1106
1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGF_Ca.
EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDL_recept_A.
Ldl_receptor_rep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asx_hydroxyl.
EGF-like.
                                                                                                                                                                                                                                                                           Repeat; Endocytosis; Glycoprotein; EGF-like domain; Coated pits;
     POTENTIAL.

CYTOPLASMIC (POTENTIAL).

LDL-RECEPTOR CLASS A 1.

LDL-RECEPTOR CLASS A 2.

EGF-LIKE 1.

EGF-LIKE 3.

EGF-LIKE 3.

EGF-LIKE 3.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 4.

LDL-RECEPTOR CLASS A 5.

LDL-RECEPTOR CLASS A 5.

LDL-RECEPTOR CLASS A 5.

LDL-RECEPTOR CLASS A 6.

LDL-RECEPTOR CLASS A 6.

LDL-RECEPTOR CLASS A 6.

LDL-RECEPTOR CLASS A 7.

LDL-RECEPTOR CLASS A 9.

LDL-RECEPTOR CLASS A 9.

LDL-RECEPTOR CLASS A 10.
                                                                                                                                                                                                            LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                     ω
                                                                                                                                   2, CALCIUM-BINDING
                                                                                                                                   (POTENTIAL)
        DISULFID
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"Surface location and high affinity for calcium of a 500-kd liver membrane protein closely related to the LDL-receptor suggest a physiological role as lipoprotein receptor."; EMBO J. 7:4119-4127(1988).
                                                              Herz J., Hamann
Stanley K.K.;
                                                                  MEDLINE=89210795; PubMed=3266596; Herz J., Hamann U., Rogne S., Myk
                                                                                                                                Ol-OCT-1996 (Rel. 34, Created)
Ol-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Low-density lipoprotein receptor-related protein 1 precursor (LRP)
(Alpha-2-macroglobulin receptor) (A2MR) (Apolipoprotein E receptor
(APOER) (CD91).
LRP1 OR A2MR.
Homo saplens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
MCBL_TaxID=9606;
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                                                               Myklebost O.,
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InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR0001881; EGF_Ca.
InterPro; IPR002172; LDL_recept_A.
InterPro; IPR000233; Ldl_recept_Oren; PF00008; EGF; 161.
Pfam; PF00005; ldl_recept_a; 31.
Pfam; PF00055; ldl_recept_b; 33.
PDITMMC. TRANSITE STATES STA
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J. Biol. Chem. 274:14130-14136(1999).

C. -!- FUNCTION: INVOLVED IN THE PLASMA CLEARANCE OF CHYLOMICRON REMNA CLEARANCE OF CHYLOMICRO REMNA CLEARANCE OF CHYLOMICRON REMNA CLEARANCE OF CHYLOMICRO REMNA CHYLOMICRO REMNA CLEARANCE OF CHYLOMICRO REMAIN CHYLOMICRO REMAIN CHYLOMICRO REMNA CLEARANCE OF CHYLOMICRO REMAIN CHYLOMICRO REMNA CLEARANCE OF CHYLOMICRO REMAIN CHYLOMICRO REMNA CLEARANCE OF CHYLOMICRO REMAIN CHYLOMICRO REMNA CLEARANCE OF CHYLOMICRO REMNA CLEARANCE OF CHYLOMICRO REMNA CLEARANCE OF CHYLOMICRO REMAIN CHYLOMICRO REMNA CLEARANCE OF CHYLOMICRO REMNA CLEARANCE OF CHYLOMICRO REMAIN CHYLOMICRO REMNA CLEARANCE OF CHYLOMICRO REMNA CHYLOMICRO REMNA CLEARANCE OF CHYLOMICRO REMAIN CHYLOMICRO REMNA 
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EMBL; AF058427; AAC64265.1;
PDB; 1CR8; 06-JAN-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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MEDLINE-90269210; PubMed-2112085;

Herz J., Kowal R.C., Goldstein J.L., Brown M.S.;

"Proteolytic processing of the 600 kd low density lipoprotein for the following strains of the fol
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"Evidence that the newly cloned low-density-lipoprotein receptor
related protein (LRP) is the alpha 2-macroglobulin receptor.";
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Van Leuven F., Stas L., Thiry E., Nelissen B., Miyake Y.;
"Strategy to sequence the 89 exons of the human LRP1 gene coding the lipoprotein receptor related protein: identification of one expressed mutation among 48 polymorphisms.";
Genomics 52:138-144(1998).
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MEDLINE-95203893; PubMed=7534747;
Van Leuven F., Stas L., Hilliker C.,
Overbergh L., Torrekens S., Moechars
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SIMILARITY: CONTAINS 31 LDL-RECEPTOR CLASS A DOMAINS.
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SMART; SM00179; EGI
SMART; SM00001; EGEI
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SMART; SM00135; LY;
PROSITE; PS00010; A
PROSITE; PS01086; E
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; SM00001; EGF_11
; SM00192; LDLa;
; SM00135; LY; 32
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PS01186; EGF_2; 8.
PS01187; EGF_CA; 2.
PS01209; LDLRA_1; 27.
PS00068; LDLRA_2; 31.
PS50068; LDLRA_2; 31.
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EGF_like;
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EGF-like
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LLDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 6.
LDL-RECEPTOR CLASS A 7.
LDL-RECEPTOR CLASS A 9.
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CYTOPLASMIC (POTENTIAL).
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    CALCIUM-BINDING
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SEQUENCE FROM N.A.
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              STRAIN-cv. Columbia;
                                 SEQUENCE FROM N.A.
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9S707;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
FICOWERING LOCUS C protein (MADS box protein FLOWERING LOCUS F).
FIC OR FIE OR AT5610140 OR T31P16_130.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
repressor of flowering.";
Plant Cell 11:949-956(1999).
[3]
                                                                                                              STRAIN-cv. C24, and cv. Columbia;
MEDLINE=99172058; PubMed=10072403;
Sheldon C.C., Burn J.E., Perez P.P., Metzger J., Edwards J.A.,
Peacock W.J., Dennis E.S.;
"The FLF MADS box gene: A repressor of flowering in Arabidopsi:
regulated by vernalization and methylation.";
Plant Cell 11:445-458(1999).
                          MEDLINE-99264314; PubMed-10330478;
Michaels S.D., Amasino R.M.;
"FLOWERING LOCUS C encodes a novel MADS domain repressor of flowering.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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BY SIMILARITY,
BY SIMILARITY
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.6e+02;
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                                              protein that acts
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RA Tabata S. Kaneko T. Nakamura Y. Kotani H., Kato T., Asamizu E.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
RA Hubarmann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
RA Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
RA Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
RA Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
RA Habermann K., Murray J., Sekhon M., Armstrong J., Becker M.,
RA Habermann K., Korisuez M., Courtney L., Courtney M., Dante M.,
RA Wagner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,
RA Wagner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.,
RA Waltensen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
RA Kingham K.-D., Wambutt R., Duesterhoeft A., Miller B., Marra M.,
RA Volckaert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,
RA Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,
RA Van Staveren M., Dirkse W., Mooljman P., Klein Lankhorst R.,
RA Van Staveren M., Dirkse W., Mooljman P., Klein Lankhorst R.,
RA Valchama V., Lamberth S., Villarroel R., Gielen J., Ardiles W.,
Sequence and analysis of chromosome 5 of the plant Arabidopsis
                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               central role in the regulation of flowering time in the late-
flowering phenotype by interacting with 'FRIGIDA', the autonomous
repressing 'SUPPRESSOR OF OVEREXERESSION OF CONSTANS 1'.

TISSUE SPECIFICITY: HIGH EXPRESSION OF CONSTANS 1'.

TOUNG TISSUE AND LOWER EXPRESSION IN THE VEGETATIVE APEX AND IN
YOUNG TISSUE OF THE INFLORESCION.

IN YOUNG TISSUES OF THE INFLORESCION.

OEVELOPMENTAL STAGE: FOUND IN SHOOTS OF NON-FLOWERING PLANTS GROWN
UNDER LONG-DAY CONDITIONS AT DAYS 4 TO 15, AND IN SHOOTS OF PLANTS
GROWN UNDER SHORT-DAY CONDITIONS AT DAYS 4 TO 11 AFTER
                                                                                                                                                                                                                                                                  ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Loss of flowering locus c activity eliminates the late-flowering phenotype of frigida and autonomous pathway mutations but not plant Cell 13:935-942(2001).
                                                                                                                                                                                                                                                                                                            77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20202708; PubMed=10716723; Sheldon C.C., Rouse D.T., Finnegan E.J., Peacock W.J., D"The molecular basis of vernalization: the central role LOCUS C (FLC).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=cv. Columbia;
MEDLINE=21178818; PubMed=11283346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 408:823-826(2000).
                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
                                                                                                                                                                                                                                                                           INDUCTION: EPIGENETICALLY DOWNREGULATED BY VERNALIZATION. SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCR.
                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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AF116528; AAD21249.1; -. AF116527; AAD21248.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acad. Sci. U.S.A. 97:3753-3758(2000).
                                                                                                                                                                                                                                                                      DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dennis E.S.;
e of FLOWERING
                                                                                                                                                       a collaboration
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GAK_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00107; PROTEIN_KINASE_ATP; PARTIAL.
PROSITE; PS00108; PROTEIN_KINASE_ST; PARTIAL.
PROSITE; PS50011; PROTEIN_KINASE_DOM; PARTIAL.
PROSITE; PS00636; DNAJ_1; PALSE_NEG.
                                                                                 EMBL; BC003958; AAH03958.1; -. InterPro; IPR001623; DnaJ.N. InterPro; IPR000719; Buk_pkinase. InterPro; IPR0002290; Ser_thr_pkin
                                                           Pfam; PF00226; DnaJ; 1
SMART; SM00271; DnaJ;
                                                                                                                                             use by non-profit institute. There are no rest
modified and this statement is not removed. Usage by are
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                              between the Swiss Institute of Bioinfo
the European Bioinformatics Institute
                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                  Submitted (PEB-2001) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Associates with cyclin G and CDK5. Seems to act as a auxilin homolog that is involved in the uncoating of clathrin-coated vesicles by Hsc70 in non-neuronal cells. Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cyclin G-associated kinase (EC 2.7.1.-) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAK_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q99KY4;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Developmental protein; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00350; MADS_BOX_1; FALSE_NEG. PROSITE; PS50066; MADS_BOX_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                             focals adhesions (By similarity).

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
SIMILARITY: CONTAINS 1 J DOMAIN.
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Pfam; PF01486; K-box; 1.
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InterPro; IPR002487; TF_Kbox
InterPro; IPR002100; TF_MADS;
                                                                                                                                                                                                                                                                                         SIMILARITY).
SUBCELLULAR LOCATION: Localizes to the perinuclear area and to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL356332; CAB
HSSP; P11746; IMNM.
                                                                                                                                                                                                                                                                                     trans-Golgi network. Also seen on the plasma
                                                                                                                                                                                                                                                                                                                         oscillates slightly during the cell cycle, peaking at GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                 Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 KW;
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50.0%;
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DNAK_BACME
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Best Local (
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GGPS_PSEAG
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NON_TER
DOMAIN
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glucosylglycerol-phosphate synthase (EC 2.4.1.213) (Glucosyl-glycerol-phosphate synthase) (GGPS).
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: Involved in salt tolerance by producing GG-phospha from ADP-glucose and glycerol-3-phosphate (G3P), an intermed in the synthesis of the osmolyte glucosy1qlycerol (GG).
-i- CATALYTIC ACTIVITY: ADP-glucose + sn-glycerol 3-phosphate - (beta-D-glucosy1)-sn-glycerol 3-phosphate + ADP-pATHMAY: Glucosy1)-sn-glycerol brynthesis; first step.
-i- PATHMAY: Glucosy1glycerol brosynthesis; first step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas anguilliseptica.
Bacteria; Proteobacteria; ga
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                                                                                                                                                                                                                   InterPro; IPRO01830; GT_20.
Pfam; PF00982; Glyco_transf_20; 1.
Transferase; Glycosyltransferase.
SEQUENCE 500 AA; 56849 MW; DOB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucosylglycerol-phosphate-synthase from heterotrophic bacteria.in
preparation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hagemann M., Steinbruch R.; "Isolation and characterization of a
DNAK_BACME
P05646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-OAl46;
                                                                                                                                                                                                                                                                                 EMBL; AJ318784; CAC50077.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=53406;
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les 8; Conserv
                                                                                             23 PTSPNGIIPTLLSF 36
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                STANDARD;
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61.5%;
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50.0%;
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Pred. No. 48;
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                PRT;
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                604 AA
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DNAK.
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16-OCT-2001 (Rel. 4
15-JUN-2002 (Rel. 4
Chaperone protein c
                                                                                                                                                                                                                                                                                                                                                                                                                                      Chaperone;
INIT_MET
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequence of a Bacillus megaterium gene homologous to the dnaK gene of Escherichia coli.";
Nucleic Acids Res. 15:3923-3923(1987).
-!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
-!- INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
        Watanabe K., Iwashiro T., Suzuki Y.;
"Features of dnaK operon genes of the obligate thermophile
thermoglucosidasius KP1006.";
Antonie Van Leeuwenhoek 77:241-250(2000).
-!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
                                                                                                                                                                                Q9KWS7;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
                                                                                                                                                                                                                                                                  BACTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sussman M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87231083; PubMed=3035506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus megaterium.
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                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                    protein) (HSP70).
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                                                                            STRAIN-KP1006;
                                                                                                               NCBI_TaxID=1426;
                                                                                                                               Bacteria; Firmicutes;
                                                                                                                                          Bacillus thermoglucosidasius
                                                                                                                                                         DNAK
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INDUCTION: BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF00012; HSP70;
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          604 AA;
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172
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40, Last sequence update)
41, Last annotation update)
41, Last annotation 100 (Heat shock 70 kDa
STRESS CONDITIONS
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43.8%;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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No.
E.G. HEAT SHOCK (BY
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SIMILARITY).
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[2]
SEQUENCE FROM N.A.
SPECIES-L.1.lactis; S
            SPECIES-L.1.lactis; STRAIN-IL1403;
MEDLINE-21235186; PubMed=11337471;
Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403.",
Genome Res. 11:731-753(2001).
                                                                                                                                         MEDLINE-94237496; PubMed-8181763; Barril M.J.S., Kim S.G., Batt C.A.; "Cloning and sequencing of the Lactococcus lactis subsp. lactis dnak gene using a PCR-based approach."; Gene 142:91-96(1994).
          -!- FUNCTION:
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uery Match
                                                                                                                                                                                                                                                               "Cloning and sequence analysis of the dnak gene region of Lactococcus J. Gen. Microbiol. 139:3253-3263(1993).
                                                                                                                                                                                                                                                                                                                 MEDLINE=94172317; PubMed=8126443; Eaton T.J., Shearman C.A., Gasson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS: PRO0301; HEATSHOCK70.
ProDom; PD000089; Hsp70; 1
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                                                        SPECIES-L.1
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             Lactococcus lactis (subsp. lactis) (Streptococcus lactis), and Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chaperone protein protein) (HSP70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P42368; 09CGY8;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seg-
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNAK OR LL0954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chaperone; ATP-binding; Heat shock; Phosphorylation.
INIT_MET 0 0 BY SIMILARITY.
MOD_RES 168 168 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SEQUENCE 606 AA; 65951 MW; 7955FD33D8845F56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNAK_LACLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426 DIPPAPRGVPQIEVTF 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB017035; BAB03215.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001023; Hsp70. Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DLPMSPRGVIASNLXF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P04475; 1DG4
                                                                                                                                                                                                                                                                                                                                                cremoris; STRAIN=MG1363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
         ΑS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32, Last sequence update)
41, Last annotation update)
dnaK (Heat shock protein 70)
                                                                                                                                                                                                                            STRAIN=LM0230;
   A CHAPERONE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.1%;
43.8%;
                                                                                                                                                                                                                                                                                                                 Gasson M.J.;
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Pred. No. 6
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SIMILARITY)
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DNAK_STRPN
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Best Local (
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                                                                  FEMS
STRAIN-TIGR4;
                                                                                 Streptococcus
                                                                                                            MEDLINE=98231633; PubMed=9570114; Kim S.-W., Choi I.-H., Kim S.-N.,
                   SEQUENCE FROM N.A.
                                                                                                                                                                 STRAIN=Rx / CP1200;
                                                                                                                                                                                                                                                                                                                                                                                                                                     P95829; 066035; FALL OV AA.
15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chaperone protein dnak (Heat shock protein 70)
DNAK OR SP0517.
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae
                                                                                                                                                                                                               Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                         pneumoniae.
                                                                                                                                                                                                                                                                      Rioux C.R., Martin D.,
"Heat shock protein HS
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes;
                                                                                      "treptococcus oneumoniae": "Kim S.-N., Kim Y.-H., Pyo S.-N., "Treptococcus oneumoniae": "Treptococcus 
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1313;
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MOD_RES
VARIANT
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VARIANT
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PROSITE; PS01036;
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ProDom; PD000089; Hsp70; 1.
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HSSP; P04475; 1DG4
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                                                       Microbiol. Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DLPMSPRGVIASNLXF 16
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607
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                                                                               pneumoniae
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HSP70_1; 1.
HSP70_2; 1.
HSP70_3; 1.
                                                                                                                                                                                                                                                  HSP70 and amino terminus of DnaJ of Streptococcus
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103
223
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592
                                                  161:217-224(1998).
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37.58;
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                                                                                                                                                                                                                                                                               Hamel J., Brodeur B.R.;
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G -> A (IN STRAIN IL1403).
D -> E (IN STRAIN IL1403).
SE -> GQ (IN STRAIN IL1403).
G -> A (IN STRAIN IL1403).
A -> D (IN STRAIN IL1403).
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Pred. No. 60;
4; Mismatches 6
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                                                                               Rhee D.-K.;
dnaK in
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MOD_RES 173

CONFLICT 493

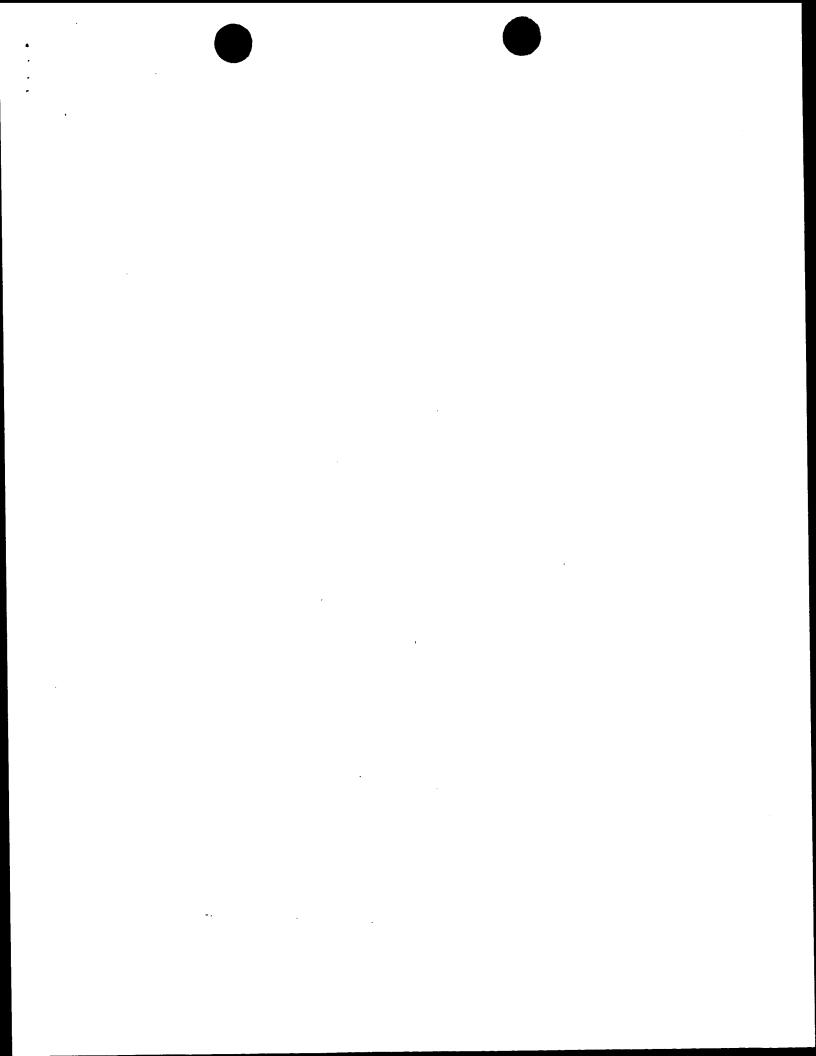
CONFLICT 495

CONFLICT 530

CONFLICT 560

CONFLICT 601

SEQUENCE 607 AA;
                                                                                                                                                                                                                                                                 tches
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PROSITE; PS00329;
PROSITE; PS01036;
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ProDom; PD000089; Hsp70; 1.
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                                                                                                                       431 DIPANPRGIPQIEVTF 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chaperone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001023; Hsp70. Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - PINCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
- I INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).
- I SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; SP0517;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 293:498-506(2001).
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                                                                                                                                                                                                                                                          Local Similarity es 6; Conserv
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HSP70_1; 1.
HSP70_2; 1.
HSP70_3; 1.
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493
495
530
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602
                                                                                                                                                                                                                                                                                                                                                                                     64842 MW;
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37.5%;
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                                                                                                                                                                                                                                                                                     Score 37; DB 1; Length 607; Pred. No. 60;
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A -> P (IN REF. 2).
A -> S (IN REF. 1).
A -> P (IN REF. 2).
T -> A (IN REF. 1 AND 2).
DG -> E (IN REF. 2).
; 11D625F1837D0760 CRC64;
                                                                                                                                                                                                                                                   Mismatches
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Minimum DB
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB ID
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77
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                                                       092580
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Q9D5U4
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Q9d5u4 mus musculu
Q9d5v1 mus musculu
Q808m0 agrobacteri
Q17051 ascaris lum
O9n9z1 drosophila
O92580 homo sapien
O943r9 oryza sativ
O943r8 oryza sativ
O91153 notophthalm
O8s724 oryza sativ
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P97961 cylindrotri
090235 ambystoma m
09hpm4 halobacteri
0974b5 sulfolobus
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SEQUENCE FROM N.A.
MEDLINE-97269074; PubMed-9111074;
Hansen O.C., Stougaard P.;
"Hexose oxidase from the red alga Chondrus crispus. Purification, molecular cloning, and expression in Pichia pastoris.";
T Biol._Chem. 272;11581-11587(1997).
Q9D5U4 PRELIMINARY;
Q9D5U4;
Q1-JUN-2001 (TremBLrel. 17,
01-JUN-2001 (TremBLrel. 17,
                                                                                                                                                                                     SEQUENCE
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01-MAY-1997 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                             Chondrus crispus (Carragheen).
Eukaryota; Rhodophyta; Florideophyceae; Gigartinales; Gigartinaceae;
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Kuchlarelli R., Barsh G.,
Balake J., Boffelli D., Bojunga N., Carninci P., Gebonaldo M.F.,
Blake J., Boltdo T., Fletcher C., Fujita M., Gariboldi M.F.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
Gustincich S., Hill D., Hofmann M., Rodriguez I., Sakamoto N.,
Gustincich S., Hill D., Ringwald M., Rodriguez I., Sakamoto N.,
Saeaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Kawai J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUE-TESTIS; MEDLINE=21085660; PubMed=11217851;
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Pfam; PF00022; actin; 1.
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Nature 409:685-690(2001).
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Rodentia;
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                              Complete
                                                                                                            Agrobacterium tumefaciens C58 Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almada N.F. Jr., Woo L. Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., W. Z., Romero P., Gordo Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sato K., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                        Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houniel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sarcosine oxidase gamma subunit. SOXG OR ATU4070 OR AGR_L_1572.
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EMBL; AK014908; BAB29615.1;
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                                                      AE009338; AAL44871.1; AE008277; AAK89359.1;
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                        proteome.
184 AA;
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19159 MW;
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81.8%;
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21, Last sequence up
21, Last annotation
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Pred. No.
                                                                                                                                                   pathogen and
73D49565A448580B CRC64;
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                                                                                                                                                                  biotechnology agent
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RESULT
Q17051
RESULT Q8XBZ9 ID Q8XBZ9 ID Q8 AC Q8 AC Q8 DT 011 DT 011 DT 011 DT 011 DT 011 DT 01 EB COC EB COC ES SCOOK RN [1]
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Q17051;
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SEQUENCE FROM N.A.
MEDLINE-95047480; PubMed-7525414;
MEDLINE-95047480; PubMed-95047480; PubMed-95047480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21, Gag protein
                                                                                                       Orf, hypothetical protein.
YIDR OR 25185 OR ECS4629.
Escherichia coli 0157:H7.
                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR005312; Peptidase_A16.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF03564; Peptidase_A16; 1.
PRINTS; PR00939; C2HCZNFINGER.
SMART; SM00343; Znf_C2HC; 2.
SEQUENCE 631 AA; 70684 MW; DBDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1994) to the EMBL/GenBank/DDBJ EMBL; Z29712; CAA82797.1; -. MEROPS; A16.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ascaris lumbricoides (common Eukaryota; Metazoa; Nematoda; Ascarididae; Ascaris.
  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                      Q8XBZ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure and genomic org
partially eliminated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aeby P., Spicher A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 149:219-225(1994).
                                                                   Escherichia
                                                                                      Bacteria; Proteobacteria;
                                                                                                                                                                                                                                               Q8XBZ9;
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                                       NCBI_TaxID-83334;
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8; Conserv
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A., de Chastonay Y., Mueller F., Tobler H
nomic organization of proretrovirus-like
ted from the somatic genome of Ascaris
                                                                                                                                                                                                                                                                                                                                                                                  445
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57.1%;
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Nematoda; Chromadorea;
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                                                                                      gamma
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Pred. No.
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                                                                                      subdivision; Enterobacteriaceae;
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3.3;
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the parasitic nematode Ascaris
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Best Local
             Query Match
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                                                                                               InterPro; IPR001242; Condensatn.
InterPro; IPR00380; Ppantne_attach.
Pfam; PF00501; AMP-binding; 2.
Pfam; PF00568; Condensation; 1.
Pfam; PF00550; pp-binding; 1.
Pfam; PF00154; AMPBINDING.
PROSITE; PS00175; ACP_DOMAIN; 1.
PROSITE; PS00455; AMP_BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Ananthazaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533(2001).
                                                                                                                                                                                                                   "Identification of genes encoding for peptide synthetas negative bacteria and filamentous fungi."; Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases EMBL; x96559; CAA65395.1; -. HSSP; P14687; IAMU. InterPro; IPR000873; AMP-bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyame Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                             Cylindrotrichum oligospermum.
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                                                                                                                                                                                                                                                                                                                        STRAIN-NRRL 18230;
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MEDLINE=21156231; PubMed=11258796;
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                                           SEQUENCE
                                                                        NON_TER
                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                              Bernhard
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=72418;
                                                                                                                                                                                                                                                                                                                                                                                      Cylindrotrichum.
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Similarity
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                                                                                      PS00012;
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1051
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                                                                                      PHOSPHOPANTETHEINE; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46314 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.28;
46.78;
53.2%;
                                           116526
                                           MW;
Score 41;
Pred. No.
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                                           7CB926576B2F0619 CRC64;
                                                                                                                                                                                                                                                                             for peptide synthetases
fungi.";
 1.1e+02;
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             Length 1051;
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SEQUENCE FROM N.A.

MEDILINE=20504483; PubMed=11016950;

Ng W.V., Kennedy S.P., Mahairas G.G., Berguist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Goo Y.A.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Maddocks D.G., Jablonski P.E., Frebs M.P., Spudich J.L., Jung K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 229 AA; 25550 MW; 81BAD98CF8FEE015 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
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Q9N921;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sec
01-JUN-2002 (TrEMBLrel. 21, Last an
                           Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Tra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of an aerobic thermoacidophilic. Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001)
EMBL; AP000983; BAB65745.1;
EMBL; AP000983; BAB65745.1;
InterPro; IPR000674; Aldxan_dh_C.
InterPro; IPR000674; Aldxan_dh_C.
InterPro; IPR001993; Mitoch_Carrier.
Pfam; PF01315; Ald_xan_dh_C; 1.
Pfam; PF02738; Ald_xan_dh_C; 1.
PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
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01-DEC-2001
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Sekine M., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.
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STRAIN=JCM 10545 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=111955;
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Ebhardt H., Lowe T.M.,
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      Metazoa; /
Neoptera;
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682 AA; 7,
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(TrEMBLrel. 21,
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  Arthropoda; Tra; Endopterygota;
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74690 MW; 863B40E9B318AA6F CRC64;
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70.0%;
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Pred. No.
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Pred. No.
                    Tracheata;
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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  Diptera;
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65;
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                       Hexapoda;
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Brachycera;
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                       Insecta;
Muscomorpha;
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Pfam;

PF00046; homeobox;

IPR001827; Antennapedia. IPR001356; Homeobox.

EMBL; D82577; HSSP; P14653;

1872

BL; D82577; BAA11574.1;

NUCLEAR

axolot1.";

InterPro;

InterPro;

TISSUE=REGENERATING BLASTEMA;

SEQUENCE FROM N.A.

NCBI_TaxID=8296; Amphibia; Batrachia; Ambystoma mexicanum Msx1 protein. 01-MAR-2002

Koshiba K., Yamamoto H.,

"Expression of Msx genes

Tamura K., Ide H., in regenerating an

and

PRINTS; PR00025; ANTENNAPEDIA.
PRINTS; PR00024; HOMEOBOX.
Probom: PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.

OCCORDIDAN OCCORDIDAN

Eukaryota; Metazoa;

m (Axolotl). ; Chordata; C a; Caudata; S

Q90235 Q90235;

229

01-NOV-1996

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel. PRELIMINARY;

01, 01, 20,

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|||:|| LPMTPRVAHLSNLGF 950

Matches

9;

Conservative

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MPMSPMGLYAAHMGY 223

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Q9HPM4; Q9HPM4; 01-MAR-2001

PRELIMINARY;

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01-MAR-2001 (TrEMBLrel. 01-MAR-2001 (TrEMBLrel. 01-MAR-2001 (TrEMBLrel.

16, 16,

Created)

Query Match Best Local S Matches 6

Local Similarity

51.9%; 40.0%;

Score Pred.

Mismatches

ŏ. 40;

ДВ 36;

Conservative

Halobacterium sp. (stra: Archaea; Euryarchaeota;

Halobacteriaceae; NCBI_TaxID=64091;

Halobacterium. (strain

in NRC-1). Halobacteria;

Vng1564h. VNG1564H.

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Q92580
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Q943R
ID Q943R
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Q943R9;
01-BEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-DEC-2001 (TrEMBLrel. 19, L
OSJNBA0083M16.17 protein.
OSJNBA0083M16.17.
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Q1-FEB-1997 (TrEMBLrel. 02, Created)
Q1-FEB-1997 (TrEMBLrel. 02, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
KIAA0258 protein (Fragment).
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"Drosophila melanogaster non-LTR retrotransposon pilger.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ278684; CAB99192.1;
FlyBase; FBg00041726; pilger\pol.
InterPro; IPR005135; Exo_endo_phos.
InterPro; IPR005135; Exo_endo_phos.
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MEDLINE-97191544; PubMcd-9039502;
MEDLINE-97191544; PubMcd-9039502;
Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y.
Tanaka A., Kotani H., Miyajima N., Nomura N.;
Trediction of the coding sequences of unidentified human
the coding sequences of 80 new genes (KIAA0201-KIAA0280) d
analysis of cDNA clones from cell line KG-1 and brain.";
DNA Res. 3.321-329(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIAAO268.
HOmo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03372; Exo_endo_phos; 1.
Pfam; PF00078; rvt; 1.
RNA-directed DNA polymerase.
SEQUENCE 989 AA; 110315 MW;
                    Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q92580
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSPOSON-PILGER NON-LTR RETROTRANSPOSON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ephydroidea; Drc
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                             μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PMSPRGVIAS
                                                                                                                                                                                                                                     DLPLHPRGFLPGHAPF 1128
                                                                                                                                                                                                                                                                           DLPMSPRGVIASNLXF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLSPRGLVAA 956
                                                                                                                                                                                                                                                                                                                                                                                                                     D87742; BAA13448.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 6; Conserv
   Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                     1193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                51.9%;
43.8%;
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60.0%;
                                                                                                                                                                                                                                                                                                                                                                                     133704 MW;
 Streptophyta;
                                                                                                             Created)
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                                                                         Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                              Score 40; DB 4;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 5;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohira M., Kawarabayasi Y.,
                                                                                                                                                                                                                                                                                                                                                                                     70FB2542F9998038 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1193
                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                               DB 4;
 Embryophyta;
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 Tracheophyta;
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                                                                                                                                                                                                                                                                                                           RESULT 15
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
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01-DEC-2001
P0031D11.27
P0031D11.27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Oryza Sativa nipponbare(GA3) genomic clone:p0031D11.";
SEQUENCE FROM N.A.
TISSUE-MID-BUD OF REGENERATING LIMB;
MEDLINE-95218226; PubMed-7703517;
                                                                                                        Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Caudata;
                                                                                                                                                                                Transcription factor (Fragment).
                                                                                                                                                                                                                                                                         Q91153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridipiantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Oryza sativa nipponbare(GA3) genomic clone:OSJNBa0083M16.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV.
Sasaki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2001) to the EMBL; AP003214; BAB64617.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4530;
                                                                      NCBI_TaxID=8316;
                                                                                         Notophthalmus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4530;
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Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                    2 LPMSPRGV 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 AA;
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                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.6%;
87.5%;
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19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003231; BAB67893.1; -. SEQUENCE 112 AA; 12233 MW; B750B7CA83A44BD6 CRC64;
            Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptophyta; Embryophyta; Tracheophyta; yta; Lillopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence up
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Salamandroidea;
                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA, chromosome
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                                                                                                  update)
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Salamandridae;
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                                                                                                                                                                                                                                                                                                                                             Length 112;
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RESULT 16
Q85724
ID Q8572
AC Q8572
AC Q8572
AC Q8572
DT 01-JU
DT 01-JU
DT 01-JU
DT U1-JU
DT U
  RESULT 17
Q91152
ID Q9115
AC Q9115
DT 01-NC
DT 01-NC
DT 01-MA
DE MSX-1
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Best Local
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tches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN-CV. NIPPONBARE;

Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,

Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.

Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G.,

VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenb

Salzberg S.L., White O., Fraser C.M.;

"Oryza sativa chromosome 10 BAC OSJNBb0091N21 genomic sequence.

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AC091122; AALB2695.1; -.
                                                                                                                 Q91152
Q91152;
                             01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
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PROSITE: PS00027; HOMEOBOX_1; 1.

PROSITE: PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00046; homeobox; 1. PRINTS; PR00024; HOMEOBOX. ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X82837; CAA58044.1;
HSSP; P22808; 1NK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dedifferentiation and redifferentiation of regenerating amphibian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
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Differential expression of myogenic regulatory genes and Msx-1 during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 MPMSPMGLYAAHVGY 107
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     protein.
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                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16595 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                           50.6%;
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                                01,
20,
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Last annotation updat
                                                          Last sequence update)
                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39;
Pred. No.
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                                Last annotation update)
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1; Mismatches
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9752C590F7DE4118 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
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                                                                                                                                               AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shvartsbeyn M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.";
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RESULT
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                  Query Match
Best Local
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Best Local :
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                                                                                                                                                   Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL; AP002999; BAB49500.1; -.
InterPro; IPR001145; Bac_OmpA.
InterPro; IPR001035; MotY.
Pfam; PF00691; OmpA; 1.
                                                                                                                                                                                                                                                                                            MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Kaneko T., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Matsuno A., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M. Takeuchi C., Yamada M., Tabata S.;
                                                                            PRINTS; PRO1023; NAFLGMOTY.
PROD00930; Bac_ompA; 1.
Hypothetical protein; Complete
SEQUENCE 442 AA; 47860 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein mlr2348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q98IL6;
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha su
Phyllobacteriaceae; Mesorhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q98IL6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00389; HOX; 1.
PROSITE; PS50071; HOMEOBOX_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. R. Soc. Lond., B, B. EMBL; x82395; CAA57791.1; HSSP; P14653; 1872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=REGENERATING BLASTEMA; MEDLINE=95249617; PubMed=77320 Crews L., Gates P., Brown R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhizobium loti (Mesorhizobium loti).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00024; HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regeneration."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Expression and activity of the newt Msx-1 gene in relation to limb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8316;
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                                                                                                                                                                                                                                                                              "Complete genome structure of the nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 MPMSPMGLYAAHVGY 274
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similarity
9; Conser
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SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 AA;
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=7732036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30966 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.6%;
40.0%;
                  50.6%;
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Score 39; DB
Pred. No. 1.1e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.
B8BBD462003CA87B CRC64;
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                                                                      proteome.
4853A307B1D71850 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subdivision;
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                                       DB 16;
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                    .1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 280;
                                     Length 442;
                                                                                                                                                                                                                                                                              symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
  Indels
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(imura T.,
2;
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Gaps
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Best Local
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X59
                     Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Mlshikawa T., Nagai K., Sato H., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., "NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PLACE100763 protein (Hypothetical 50.2 kDa protein).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_hlke.
InterPro; IPR003600; Ig_hlke.
InterPro; IPR003006; Ig_hlC.
IPf6m; PF00047; Ig; 2.
SMART; SM00407; IG; 2.
SMART; SM00410; IG_llke; 1.
SMART; PS00290; IG_hRC; UNKNOWN_1.
PROSITE; PS00290; IG_hRC; UNKNOWN_1.
SEQUENCE 468 AA; 50220 MW; 7C2FC6D5744FB101 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Mlshikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., "NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                     TISSUE-PLACENTA;
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                               Q9BX59;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BX59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 50.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 NLPLSPQGTVRTAVEF 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DLPMSPRGVIASNLXF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 37.9
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.6%; Score 39; DB 4; Length 468; 37.5%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                             468 AA.
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                                                                                                        Matches
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Best Local Similarity
                                                                                                 InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 2.
SMART; SM00409; IG; 1.
SMART; SM00407; IGC1; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 468 AA; 50177 MW; 1826E2C6
                                                                                                                                                                                                              Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK002056; BAB41077.1; -.
EMBL; BC015017; AAH15177.1; -.
176 NLPLSPQGTVRTAVEF 191
                                                                                                                                                                                                                                                                          TISSUE-SKIN;
                         1 DLPMSPRGVIASNLXF 16
                                                     6;
                                                   Conservative
                                                                                                50177 MW; 1826E2C8F3C39841 CRC64;
                                                              50.6%;
                                                  6;
                                                          Score 39; DB 4; Length 468; Pred. No. 1.1e+02;
                                               Mismatches
                                                Indels
                                              0;
                                              Gaps
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Search completed: January 2, 2003, 12:07:20 Job time: 103 secs

